

WEST Search History

DATE: Monday, June 21, 2004

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
		<i>DB=USPT; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L18	L17 not l3	0
<input type="checkbox"/>	L17	L16 same l2	2
<input type="checkbox"/>	L16	catalytic adj domain	2478
<input type="checkbox"/>	L15	L14 not l3	2
<input type="checkbox"/>	L14	l2 same l13	4
<input type="checkbox"/>	L13	(c adj terminal) or (c-terminal) or (c adj terminus) or (c-terminus) or carboxyterminal or (carboxy adj terminal) or carboxyterminus or (carboxy adj terminus)	29825
<input type="checkbox"/>	L12	L2 same l7	3
<input type="checkbox"/>	L11	L2 near40 l7	0
<input type="checkbox"/>	L10	l2 near30 l7	0
<input type="checkbox"/>	L9	l2 and l7	52
<input type="checkbox"/>	L8	l2 near20 L7	0
<input type="checkbox"/>	L7	(fusion or fused) adj (protein or peptide)	18128
<input type="checkbox"/>	L6	L5 not l3	7
<input type="checkbox"/>	L5	l2 and L4	10
<input type="checkbox"/>	L4	james.in.	203604
<input type="checkbox"/>	L3	l1 and L2	3
<input type="checkbox"/>	L2	starch adj (synthase or synthetase)	197
<input type="checkbox"/>	L1	myers.in.	5098

END OF SEARCH HISTORY

Hit List

Clear	Generate Collection	Print	Fwd Refs	Blkwd Refs
Generate OACS				

Search Results - Record(s) 1 through 3 of 3 returned.

☐ 1. Document ID: US 6639125 B1

L3: Entry 1 of 3

File: USPT

Oct 28, 2003

US-PAT-NO: 6639125

DOCUMENT-IDENTIFIER: US 6639125 B1

TITLE: Dull1 coding for a starch synthase and uses thereof

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Claims	Drawings	Comments	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	----------	--------	----------	----------	----------

☐ 2. Document ID: US 6410716 B1

L3: Entry 2 of 3

File: USPT

Jun 25, 2002

US-PAT-NO: 6410716

DOCUMENT-IDENTIFIER: US 6410716 B1

TITLE: Isolation of SU1, a starch debranching enzyme, the product of the maize gene sugary1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Claims	Drawings	Comments	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	----------	--------	----------	----------	----------

☐ 3. Document ID: US 5981728 A

L3: Entry 3 of 3

File: USPT

Nov 9, 1999

US-PAT-NO: 5981728

DOCUMENT-IDENTIFIER: US 5981728 A

TITLE: Dull1 coding for a novel starch synthase and uses thereof

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Claims	Drawings	Comments	Drawings
------	-------	----------	-------	--------	----------------	------	-----------	----------	--------	----------	----------	----------

Clear	Generate Collection	Print	Fwd Refs	Blkwd Refs
Generate OACS				

Hit List

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Search Results - Record(s) 1 through 7 of 7 returned.

☐ 1. Document ID: US 6391551 B1

L6: Entry 1 of 7

File: USPT

May 21, 2002

US-PAT-NO: 6391551

DOCUMENT-IDENTIFIER: US 6391551 B1

TITLE: Detection of nucleic acid hybrids

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	KWC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	----------

☐ 2. Document ID: US 6350934 B1

L6: Entry 2 of 7

File: USPT

Feb 26, 2002

US-PAT-NO: 6350934

DOCUMENT-IDENTIFIER: US 6350934 B1

TITLE: Nucleic acid encoding delta-9 desaturase

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	KWC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	----------

☐ 3. Document ID: US 5675064 A

L6: Entry 3 of 7

File: USPT

Oct 7, 1997

US-PAT-NO: 5675064

DOCUMENT-IDENTIFIER: US 5675064 A

TITLE: Starch and grain with a novel genotype

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	KWC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	-----	----------

☐ 4. Document ID: US 5648249 A

L6: Entry 4 of 7

File: USPT

Jul 15, 1997

US-PAT-NO: 5648249

DOCUMENT-IDENTIFIER: US 5648249 A

TITLE: Method of improving the quality of stored potatoes

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	KWIC	Draw. De
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☐ 5. Document ID: US 5648111 A

L6: Entry 5 of 7

File: USPT

Jul 15, 1997

US-PAT-NO: 5648111

DOCUMENT-IDENTIFIER: US 5648111 A

TITLE: Starch and grain with a novel genotype

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	KWIC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	------	----------

☐ 6. Document ID: US 5516939 A

L6: Entry 6 of 7

File: USPT

May 14, 1996

US-PAT-NO: 5516939

DOCUMENT-IDENTIFIER: US 5516939 A

TITLE: Starch and grain with a novel genotype

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	KWIC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	------	----------

☐ 7. Document ID: US 5502270 A

L6: Entry 7 of 7

File: USPT

Mar 26, 1996

US-PAT-NO: 5502270

DOCUMENT-IDENTIFIER: US 5502270 A

**** See image for Certificate of Correction ****

TITLE: Starch and grain with a novel genotype

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	KWIC	Draw. De
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	------	----------

Clear

Generate Collection

Print

Fwd Refs

Bkwd Refs

Generate OACS

Terms

Documents

L5 not L3

7

Display Format:

TI

Change Format

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Hit List

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Search Results - Record(s) 1 through 3 of 3 returned.

☐ 1. Document ID: US 6642437 B1

L12: Entry 1 of 3

File: USPT

Nov 4, 2003

US-PAT-NO: 6642437

DOCUMENT-IDENTIFIER: US 6642437 B1

TITLE: Production of proteins in plant seeds

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Pub. No.	Claims	RWC	Draw. Data
------	-------	----------	-------	--------	----------------	------	-----------	----------	----------	--------	-----	------------

☐ 2. Document ID: US 6639125 B1

L12: Entry 2 of 3

File: USPT

Oct 28, 2003

US-PAT-NO: 6639125

DOCUMENT-IDENTIFIER: US 6639125 B1

TITLE: Dull1 coding for a starch synthase and uses thereof

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Pub. No.	Claims	RWC	Draw. Data
------	-------	----------	-------	--------	----------------	------	-----------	----------	----------	--------	-----	------------

☐ 3. Document ID: US 5981728 A

L12: Entry 3 of 3

File: USPT

Nov 9, 1999

US-PAT-NO: 5981728

DOCUMENT-IDENTIFIER: US 5981728 A

TITLE: Dull1 coding for a novel starch synthase and uses thereof

Full	Title	Citation	Front	Review	Classification	Date	Reference	Abstract	Pub. No.	Claims	RWC	Draw. Data
------	-------	----------	-------	--------	----------------	------	-----------	----------	----------	--------	-----	------------

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Terms	Documents
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L2 same L7

3

Display Format:

TI

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Hit List

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Search Results - Record(s) 1 through 2 of 2 returned.

☐ 1. Document ID: US 6590141 B1

L15: Entry 1 of 2

File: USPT

Jul 8, 2003

US-PAT-NO: 6590141

DOCUMENT-IDENTIFIER: US 6590141 B1

TITLE: Nucleic acid molecules from plants encoding enzymes which participate in starch synthesis

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	RMIC	Draw. D
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	------	---------

☐ 2. Document ID: US 6476212 B1

L15: Entry 2 of 2

File: USPT

Nov 5, 2002

US-PAT-NO: 6476212

DOCUMENT-IDENTIFIER: US 6476212 B1

**** See image for Certificate of Correction ****

TITLE: Polynucleotides and polypeptides derived from corn ear

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	RMIC	Draw. D
------	-------	----------	-------	--------	----------------	------	-----------	--	--	--------	------	---------

Clear	Generate Collection	Print	Fwd Refs	Bkwd Refs
Generate OACS				

Terms	Documents
L14 not L3	2

Display Format:

Change Format

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=> file ca

=> 's (starch(w) (synthase? or synthetase?))/ab,bi

L1 779 (STARCH(W) (SYNTHASE? OR SYNTHETASE?))/AB,BI

=> s (dull(w)1 or du1)/ab,bi

L2 36 (DULL(W)1 OR DU1)/AB,BI

=> s l1 or l2

L3 807 L1 OR L2

=> s (carboxyterminal or carboxyterminus or c(w)terminal or c(w)terminus or carb

L4 81907 (CARBOXYTERMINAL OR CARBOXYTERMINUS OR C(W)TERMINAL OR C(W)TERMI
NUS OR CARBOXY(W)TERMINAL OR CARBOXY(W)TERMINUS)/AB,BI

=> s l3(l)l4

L5 10 L3(L)L4

=> file biosis

=> s l5

L6 7 L3(L)L4

=> dup rem

L7 10 DUP REM L5 L6 (7 DUPLICATES REMOVED)

=> d l7 1-10 ti py

L7 ANSWER 1 OF 10 CA COPYRIGHT 2004 ACS on STN
TI Chimeric genes and starch synthases with heterologous glucan-binding and
glycosyltransferase domains and transgenic plants producing altered starch
PY 2002

L7 ANSWER 2 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 1
TI An immunoenzymatic solid-phase assay for quantitative determination of
HIV-1 protease activity
PY 2002

L7 ANSWER 3 OF 10 CA COPYRIGHT 2004 ACS on STN
TI Corn starch synthase isoenzyme and cDNA, transgenic plants expressing this
cDNA, and method for production of starches
PY 2001

L7 ANSWER 4 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 2
TI Chain-length specificities of maize starch synthase I enzyme: Studies of
glucan affinity and catalytic properties
PY 2001

L7 ANSWER 5 OF 10 CA COPYRIGHT 2004 ACS on STN
TI Fusion proteins with Chlamydomonas starch synthase and food and
pharmaceuticals containing starch-fusion protein complexes
PY 2000

L7 ANSWER 6 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 3
TI The structure and expression of the wheat starch synthase III gene. Motifs
in the expressed gene define the lineage of the starch synthase III gene
family
PY 2000

C7/5
Biosis
6/21/04

L7 ANSWER 7 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 4
 TI Expression of a cassava granule-bound starch synthase gene in the
 PY amylose-free potato only partially restores amylose content
 1999

L7 ANSWER 8 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 5
 TI Specificity of starch synthase isoforms from potato
 PY 1999

L7 ANSWER 9 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 6
 TI Identification of the soluble starch synthase activities of maize
 PY endosperm
 1999

L7 ANSWER 10 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 7
 TI Isolation and characterization of the zSSIa and zSSIb starch synthase
 PY cDNA clones from maize endosperm
 1998

=> d 17 ab 5-10

=> d 17 7 bib

L7 ANSWER 7 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 4
 AN 132:247052 CA
 TI Expression of a cassava granule-bound starch synthase gene in the
 AU amylose-free potato only partially restores amylose content
 Salehuzzaman, Shah N. I. M.; Vincken, Jean-Paul; Van De Wal, Marion;
 CS Straatman-Engelen, Irma; Jacobsen, Evert; Visser, Richard G. F.
 The Graduate School Experimental Plant Sciences, Laboratory of Plant
 SO Breeding, Wageningen Agricultural University, Wageningen, 6700 AJ, Neth.
 Plant, Cell and Environment (1999), 22(10), 1311-1318
 CODEN: PLCEDV; ISSN: 0140-7791
 PB Blackwell Science Ltd.
 DT Journal
 LA English

=> d 17 9 bib

L7 ANSWER 9 OF 10 CA COPYRIGHT 2004 ACS on STN DUPLICATE 6
 AN 131:99886 CA
 TI Identification of the soluble starch synthase activities of maize
 AU endosperm
 Cao, Heping; Imparl-Radosevich, Jennifer; Guan, Hanping; Keeling, Peter
 L.; James, Martha G.; Myers, Alan M.
 CS Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State
 University, Ames, IA, 50011, USA
 SO Plant Physiology (1999), 120(1), 205-215
 CODEN: PLPHAY; ISSN: 0032-0889
 PB American Society of Plant Physiologists
 DT Journal
 LA English

=> file ca

=> s (myers, a?)/au

L8 841 (MYERS, A?)/AU

=> s 11 and 18

L9 5 L1 AND L8

=> file biosis

=> s l9

L10 8 L1 AND L8

=> dup rem

L11 9 DUP REM L9 L10 (4 DUPLICATES REMOVED)

=> d l11 1-9

L11 ANSWER 1 OF 9 CA COPYRIGHT 2004 ACS on STN DUPLICATE 1

AN 139:334824 CA

TI Protein and cDNA sequences of corn gene dull1 coding for a ***starch***
synthase and use

IN ***Myers, Alan M.*** ; James, Martha Graham

PA Iowa State University Research Foundation, Inc., USA

SO U.S., 56 pp., Cont.-in-part of U.S. Ser. No. 968,542.

CODEN: USXXAM

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	US 6639125	B1	20031028	US 2000-554467	20000512
	US 5981728	A	19991109	US 1997-968542	19971112
	WO 9924575	A1	19990520	WO 1998-US24225	19981112

L11 ANSWER 2 OF 9 CA COPYRIGHT 2004 ACS on STN DUPLICATE 2

AN 132:133950 CA

TI Purification and characterization of soluble ***starch***
synthases from maize endosperm

AU Cao, Heping; James, Martha G.; ***Myers, Alan M.***

CS Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State University, Ames, IA, 50011, USA

SO Archives of Biochemistry and Biophysics (2000), 373(1), 135-146

CODEN: ABBIA4; ISSN: 0003-9861

PB Academic Press

DT Journal

LA English

L11 ANSWER 3 OF 9 CA COPYRIGHT 2004 ACS on STN

AN 130:333760 CA

TI Maize ***starch*** ***synthase*** gene dul and uses in starch
production

IN ***Myers, Alan M.*** ; James, Martha G.

PA Iowa State University Research Foundation, Inc., USA

SO PCT Int. Appl., 138 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	WO 9924575	A1	19990520	WO 1998-US24225	19981112
	US 5981728	A	19991109	US 1997-968542	19971112
	CA 2309346	AA	19990520	CA 1998-2309346	19981112
	AU 9915236	A1	19990531	AU 1999-15236	19981112
	AU 761419	B2	20030605		
	EP 1030922	A1	20000830	EP 1998-959440	19981112
	BR 9814864	A	20011106	BR 1998-14864	19981112
	JP 2001522604	T2	20011120	JP 2000-520569	19981112
	NZ 504534	A	20021220	NZ 1998-504534	19981112
	MX 200004586	A	20001110	MX 2000-4586	20000512
	US 6639125	B1	20031028	US 2000-554467	20000512

L11 ANSWER 4 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2000:278998 BIOSIS
 DN PREV200000278998
 TI Dull1 coding for a novel ***starch*** ***synthase*** and uses
 thereof.
 AU ***Myers, Alan M.*** [Inventor, Reprint author]; James, Martha G.
 [Inventor]
 CS Des Moines, IA, USA
 ASSIGNEE: Iowa State University Research Foundation, Inc., Ames, IA, USA
 PI US 5981728 November 09, 1999

L11 ANSWER 5 OF 9 CA COPYRIGHT 2004 ACS on STN DUPLICATE 3
 AN 131:99886 CA
 TI Identification of the soluble ***starch*** ***synthase***
 activities of maize endosperm
 AU Cao, Heping; Imparl-Radosevich, Jennifer; Guan, Hanping; Keeling, Peter
 L.; James, Martha G.; ***Myers, Alan M.***
 CS Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State
 University, Ames, IA, 50011, USA
 SO Plant Physiology (1999), 120(1), 205-215
 CODEN: PLPHAY; ISSN: 0032-0889
 PB American Society of Plant Physiologists
 DT Journal
 LA English

L11 ANSWER 6 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2003:144471 BIOSIS
 DN PREV200300144471
 TI Identification and characterization of the ***starch***
 synthase activity coded for by maize gene dull1.
 AU Cao, Heping [Reprint Author]; ***Myers, Alan M.*** ; James, Martha G.
 CS Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State
 University, Ames, IA, USA
 hpcao@iastate.edu
 SO Plant Biology (Rockville), (1999) Vol. 1999, pp. 193. print.
 Meeting Info.: Annual Meeting of the American Society of Plant
 Physiologists. Baltimore, Maryland, USA. July 24-28, 1999. American
 Society of Plant Physiologists (ASPP).
 DT Conference; (Meeting)
 Conference; (Meeting Poster)
 Conference; Abstract; (Meeting Abstract)
 LA English

L11 ANSWER 7 OF 9 CA COPYRIGHT 2004 ACS on STN DUPLICATE 4
 AN 129:2125 CA
 TI Characterization of dull1, a maize gene coding for a novel ***starch***
 synthase
 AU Gao, Ming; Wanat, Jennifer; Stinard, Philip S.; James, Martha G.;
 Myers, Alan M.
 CS Department of Biochemistry and Biophysics, Iowa State University, Ames,
 IA, 50011, USA
 SO Plant Cell (1998), 10(3), 399-412
 CODEN: PLCEEW; ISSN: 1040-4651
 PB American Society of Plant Physiologists
 DT Journal
 LA English

L11 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
 AN 2003:119968 BIOSIS
 DN PREV200300119968
 TI Identification of DU1 protein as a major soluble ***starch***


```

.      ***synthase***    in maize kernels.
AU    Cao, Heping [Reprint Author]; James, Martha G. [Reprint Author];
      ***Myers, Alan M.***    [Reprint Author]
CS    Iowa State University, Ames, IA, USA
SO    Plant Biology (Rockville), (1998) Vol. 1998, pp. 119. print.
      Meeting Info.: Annual Meeting of the American Society of Plant
      Physiologists combined with the 9th International Conference on
      Arabidopsis Research. Madison, WI, USA. June 27-July 01, 1998. American
      Society of Plant Physiologists (ASPP).
DT    Conference; (Meeting)
      Conference; (Meeting Poster)
      Conference; Abstract; (Meeting Abstract)
LA    English

L11   ANSWER 9 OF 9 BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    2003:89137 BIOSIS
DN    PREV200300089137
TI    Identification of DU1 protein as a major soluble    ***starch***
      ***synthase***    in maize kernels.
AU    Cao, Heping [Reprint Author]; Mou, Beiquan [Reprint Author]; James, Martha
      G. [Reprint Author];    ***Myers, Alan M.***    [Reprint Author]
CS    Iowa State University, Ames, IA, USA
SO    Plant Biology (Rockville), (1998) Vol. 1998, pp. 25. print.
      Meeting Info.: Annual Meeting of the American Society of Plant
      Physiologists combined with the 9th International Conference on
      Arabidopsis Research. Madison, WI, USA. June 27-July 01, 1998. American
      Society of Plant Physiologists (ASPP).
DT    Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA    English

```

```
=> file ca
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=> s (james, m?)/au
L12      1148 (JAMES, M?)/AU
```

```
=> s l12 and l1
L13      5 L12 AND L1
```

```
=> s l13 not l9
L14      0 L13 NOT L9
```

```
=> file biosis
```

```
=> s l14
L15      0 L13 NOT L9
```

```
=> log y
STN INTERNATIONAL LOGOFF AT 21:07:09 ON 21 JUN 2004
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: June 20, 2004, 03:45:55 ; Search time 16042 Seconds
(without alignments)
7019.399 Million cell updates/sec
Title: US-10-634-262-1_COPY_2425_5022
Perfect score: 2598
Sequence: 1 agctgtgtgaaaaaattat.....gctgaacagggcgatctcag 2598

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pin.*
- 35: em.htg.rod.*
- 36: em.htg.man.*
- 37: em.htg.vrt.*
- 38: em.sv.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2598	100.0	6027	6	AR085480 Sequence
2	2598	100.0	6027	6	AR427878 Sequence
3	2598	100.0	6027	6	BD091317 Sequence
4	2598	100.0	6027	8	AF023159 Dull cod
5	1766.6	68.0	5346	8	AF258608 Zea may
6	1703.8	65.6	5760	6	AF258608 Triticum
7	1647.2	63.4	4241	8	AX653280 Sequence
8	1646.8	63.4	4241	8	AX122098 Oryza sat
9	1581.4	60.9	3032	6	AX654187 Sequence
10	1500.4	57.8	4121	6	AX755430 Sequence
11	1500.4	57.8	4121	6	AX353090 Sequence
12	1217.6	46.4	3901	8	AX085557 Sequence
13	1206.4	46.4	4127	8	AX225088 Vigna ung
14	1206.4	46.4	4127	8	AX63216 Sequence 3
15	1204.8	46.4	4167	8	AX94400 S.tuberosum
16	1204.8	46.4	4168	6	AX1209 Sequence 11
17	1204.8	46.4	4168	6	AR112889 Sequence
18	1204.8	46.4	4168	6	AR256404 Sequence
19	1141.2	43.9	3078	6	AX651938 Sequence
20	931	35.8	2303	6	AX1199 Sequence 1
21	931	35.8	2303	6	AR112884 Sequence
22	931	35.8	2303	6	AR256399 Sequence
23	739.4	28.5	1826	8	AK059368 Oryza sat
24	501	19.3	11550	8	AF258609 Regilops
25	485	18.7	138993	8	AP005441 Oryza sat
26	485	18.7	142044	2	AP004660 Oryza sat
27	483.4	18.6	9586	8	AX100469 Oryza sat
28	444.4	17.1	8821	8	AF432915 Oryza sat
29	444.4	17.1	187601	8	OSJN00079 Arabidops
30	271.6	10.5	91566	8	F25C20 Zea may
31	186.2	7.2	1856	6	AF023160 Sequence
32	175	6.7	212	6	AR244742 Sequence
33	147.6	5.7	3519	8	AX06752 Vigna ung
34	145	5.6	2652	6	AR3857 Sequence 1
35	145	5.6	2652	6	AR145490 Sequence
36	145	5.6	2652	6	AR392029 Sequence
37	144.8	5.6	3434	6	AR220351 Sequence
38	140.8	5.4	1275	6	AX088102 Sequence
39	140.8	5.4	1297	8	BT009276 Triticum
40	140.8	5.4	3386	8	AX044844 Triticum
41	137.6	5.3	759	6	AX756331 Sequence
42	134.4	5.2	2748	8	AX224560 Oryza sat
43	134.4	5.2	3080	8	AX373258 Oryza sat
44	134.4	5.2	3280	8	AK067577 Oryza sat
45	125.2	4.8	2865	6	AX654024 Sequence

ALIGNMENTS

RESULT 1
AR085480
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AR085480
Sequence 1 from patent US 5981728.
AR085480
GI:10012247

Unknown.
Unclassified.
1 (bases 1 to 6027)
Myers, A.M. and James, M.G.
Dull coding for a novel starch synthase and uses thereof
Patent: US 5981728-A 1 09-NOV-1999;
Location/Qualifiers

parent

linear PAT 01-SEP-2000

Db	4465	ACTACACTTGTGAGAAATGTGTTGAAGGCAAGAGGGCTGCTAAGAGGGCACTGCAGCAGA	4524
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Qy	2221	TGTTTTCGTTGCTTCAGCGCGCGGACTCTCGAATCCAAAGCTGATTTGTCAAACCTGGCGA	2280
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Qy	2281	ATACGCTCCACGCGCTAAACCATGGGCAAGTGAAGGCTTCTTGTGACCTACGACGAGCCTC	2340
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Qy	2401	GGCGCTTAATCAGCTCGTCGCCATCGGCTATGGAAACCATCCGATTTGTCGCAAGACTG	2460
Db	4825	GGCGCTTAATCAGCTCGTCGCCATCGGCTATGGAAACCATCCGATTTGTCGCAAGACTG	4884
Qy	2461	GAGGCTCTTTCGACACTGCTTCGATGTGGCAATGACAAGGAACGAGCCGAGATCGAG	2520
Db	4885	GAGGCTCTTTCGACACTGCTTCGATGTGGCAATGACAAGGAACGAGCCGAGATCGAG	4944
Qy	2521	GCTTGAGCCCAACGGGTTTAGCTTTGACGAGCTGATAGCAACGCTGTTGACTACGCGC	2580
Db	4945	GCTTGAGCCCAACGGGTTTAGCTTTGACGAGCTGATAGCAACGCTGTTGACTACGCGC	5004
Qy	2581	TGAACAGGGCGATCTCAG	2598
Db	5005	TGAACAGGGCGATCTCAG	5022
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AR427878			
LOCUS	AR427878	6027 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 1 from patent US 6639125.		
ACCESSION	AR427878		
VERSION	AR427878.1	GI:40186871	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 6027)		
AUTHORS	Myers,A.M. and James,M.G.		
TITLE	Dull1 coding for a starch synthase and uses thereof		
JOURNAL	Patent: US 6639125-A 1 28-OCT-2003;		
FEATURES	Location/Qualifiers		
source	1..6027		
	/organism="unknown"		
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Best Local Similarity 100.0%; Pred. No. 0;			
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	AGCTTGCTGAAAAAATTAATTCGCTGGGAAACAAAGTGTGTTTACTTATCCAGATGTAATGA	60
Db	2425	AGCTTGCTGAAAAAATTAATTCGCTGGGAAACAAAGTGTGTTTACTTATCCAGATGTAATGA	2484
Qy	61	AAGCTGATTCACAAATGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCAAATGAGC	120
Db	2485	AAGCTGATTCACAAATGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCAAATGAGC	2544
Qy	121	CTGATGTAATCTATCAAGGAGCATTCANTGGGTGAAGTGGAGATTTTTCCTGAAAAAT	180

Db	2545	CTGATGTAATCTATCAAGGAGCATTCANTGGTGAAGTGGAGATTTTTCATGAAAAAT	2604
Qy	181	TGCAACAAGAGGAGCTGCGAGGGACCTGGTGGTCTGCAAACTATACATTCCTTAAGCAGG	240
Db	2605	TGCAACAAGAGGAGCTGCGAGGGACCTGGTGGTCTGCAAACTATACATTCCTTAAGCAGG	2664
Qy	241	CATACAGAAATGACCTTTGTGTTTAAACGACACACCGGTATGAAATAATAACAATA	300
Db	2665	CATACAGAAATGACCTTTGTGTTTAAACGACACACCGGTATGAAATAATAACAATA	2724
Qy	301	ATGATTTTCGTGATCAAAATAGAACCCATCGGATGAAAAATTTTATTTGAGATTTCTTGG	360
Db	2725	ATGATTTTCGTGATCAAAATAGAACCCATCGGATGAAAAATTTTATTTGAGATTTCTTGG	2784
Qy	361	CTGAAGAAACCAACGAGAACTTGAAGAACCTTGAAGAACCTTGAAGAACCTTGAAGAACCTT	420
Db	2785	CTGAAGAAACCAACGAGAACTTGAAGAACCTTGAAGAACCTTGAAGAACCTTGAAGAACCTT	2844
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Db	3265	GACATGATTTTCATGCTACCTTCCAAATAAATGAGTGTGAGGAGAGTATTCGATGAG	3324
Qy	901	AAGAAACAAAGGATCTATACAGGCTTCAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGATTA	960
Db	3325	AAGAAACAAAGGATCTATACAGGCTTCAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGATTA	3384
Qy	961	AAAGGAAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAAGGAAAGAACTATGAGAA	1020
Db	3385	AAAGGAAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAAGGAAAGAACTATGAGAA	3444
Qy	1021	TGTTCTCTGGTTCTCAGAAACAACTTGTGTTTACACCGAACCCACTTGAATACATGCTGGAA	1080
Db	3445	TGTTCTCTGGTTCTCAGAAACAACTTGTGTTTACACCGAACCCACTTGAATACATGCTGGAA	3504
Qy	1081	CTACTATTGATGCTGCTTAAATCCCTTCTAAATCCCTTCTAAATCCCTTCTAAATCCCTTCT	1140
Db	3505	CTACTATTGATGCTGCTTAAATCCCTTCTAAATCCCTTCTAAATCCCTTCTAAATCCCTTCT	3564
Qy	1141	GGTTTTCGATGCTCTTAAATCCCTTCTAAATCCCTTCTAAATCCCTTCTAAATCCCTTCT	1200
Db	3565	GGTTTTCGATGCTCTTAAATCCCTTCTAAATCCCTTCTAAATCCCTTCTAAATCCCTTCT	3624
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4045 AACCTCAAAATGGGATGTTGGAGTCGATATGATATGAGGAGCAATGACGCGCAT 4104
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4165 TAATACATTTGCATGATGTTCAAGTCTCTGTTGCTGCTGCTACACAAGGAAACTACG 4224
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1861 CGCATCATATTTGGCAACGATGATGATGATAAGCAACACTGCTCTAATACAT 1920
4285 CGCATCATATTTGGCAACGATGATGATGATAAGCAACACTGCTCTAATACAT 4344
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4345 ATTCAAGGAAGTGTGAGTCTAGTGTGCTATGTTCTCTCATCTTGGGAATTTCTATGCA 4404
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2041 ACTACACTTGTGAGATGTTGTTGAAGGCAAGAGGCTGCTAAGAGGCACTGACACAGA 2100
4465 ACTACACTTGTGAGATGTTGTTGAAGGCAAGAGGCTGCTAAGAGGCACTGACACAGA 4524
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4525 AGTTTGGGTTTACAGCAATTCGATGTTCCCGTCTAGGAATTCGTACTCGCTGACAGCCC 4584
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RESULT 3
BD091317
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD091317 6027 bp DNA linear PAT 27-AUG-2002
Dull1 coding for a novel starch synthase and uses thereof.
BD091317
BD091317.1 GI:22636927
JP 2001522604-A/1.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 6027)
Myers,A.M. and James,M.G.
Dull1 coding for a novel starch synthase and uses thereof
Patent: JP 2001522604-A 1 20-NOV-2001;
IOWA STATE UNIVERSITY RESEARCH FOUNDATION INC
OS Zea mays (maize)
PN JP 2001522604-A/1
PD 20-NOV-2001
PF 12-NOV-1998 JP 2000520569
PR 12-NOV-1997 US 08/968542
PI ALAN M MYERS, MARTHA G JAMES
PC
C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12P19/04,C12N15/00,C12N5/ PC
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CC enzyme DUL1.
CC synthase
CC Location/Qualifiers
FH Key 1..6027
FT source /organism='Zea mays (maize)'.
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source
1..6027
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	181	TGCA	CAAGACG	AGCTGG	CAGGGGA	CTGGTGGT	GTGCAAACTATA	CTTCTTAAGCAGG	240
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QY	301	ATGATTT	TCGTGATA	CAAAATAG	AAAGCACC	ATGGATGAAA	ATTTATTTCAGGAT	TTCCTTGG	360
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QY	1081	CTACTAT	TGATGCT	TTTTATAT	CTCTCT	TAATACAG	TTTCTAACT	TGGAAAGCCAGAGGTTT	1140
DB	3505	CTACTAT	TGATGCT	TTTTATAT	CTCTCT	TAATACAG	TTTCTAACT	TGGAAAGCCAGAGGTTT	3564
QY	1141	GGTTTT	CGATGTT	CTCTTTT	TAATTC	GTGATG	TATCC	AGGTGGGGTGTTC	1200
DB	3565	GGTTTT	CGATGTT	CTCTTTT	TAATTC	GTGATG	TATCC	AGGTGGGGTGTTC	3624
QY	1201	TGATCA	AGCAGAA	AAATGG	TTTCA	CTTAAAG	CAACAG	TTTTCGTTCCACGAGATGCCT	1260

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3685	Db	ATATGATGGACTTCGTTTTTCTCGGAGTCAGAAGAGGTGGAATTTATGATTAACAGAAATG	3744
1321	QY	GGTTAGACTATCATATTCCTGTTTTTGGTCAATTGCAAGGACCCACTATGCACATG	1380
3745	Db	GGTTAGACTATCATATTCCTGTTTTTGGTCAATTGCAAGGACCCACTATGCACATG	3804
1381	QY	TCCACAAATGCTGTGAGATGCGACCAATCGAAAGGTTGGAGGCTTCGCTGATGTTGTCA	1440
3805	Db	TCCACAAATGCTGTGAGATGCGACCAATCGAAAGGTTGGAGGCTTCGCTGATGTTGTCA	3864
1441	QY	CTAGTCTTTTCACTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATCTTTCCAAAGT	1500
3865	Db	CTAGTCTTTTCACTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATCTTTCCAAAGT	3924
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3925	Db	ACGGTTGCTTGAATCTAAGCAATGTCAAGAATCTACAAATCCATCAGAGTTTTCTTCGG	3984
1561	QY	GTGGTTCTGAAATTAATATGTGTGGCGTGGACTAGTCAAGGCGCTTTGTGTTACTTCTCTGG	1620
3985	Db	GTGGTTCTGAAATTAATATGTGTGGCGTGGACTAGTCAAGGCGCTTTGTGTTACTTCTCTGG	4044
1621	QY	AACCTCAAAATGGGATGTTTGGAGTCGGATATGATATGCGAGGACGATGACCGCGAT	1680
4045	Db	AACCTCAAAATGGGATGTTTGGAGTCGGATATGATATGCGAGGACGATGACCGCGAT	4104
1681	QY	TTGGCTTCTTCTGTGCTGTCTCTAGAGTTTCTCTCCCAAAGTGGATCTTCTCCGAACA	1740
4105	Db	TTGGCTTCTTCTGTGCTGTCTCTAGAGTTTCTCTCCCAAAGTGGATCTTCTCCGAACA	4164
1741	QY	TAATACATTTGCCATGATTTGCTCAAGTCTCCTGTGCTGGCTACACAAGGAAAACTAGC	1800
4165	Db	TAATACATTTGCCATGATTTGCTCAAGTCTCCTGTGCTGGCTACACAAGGAAAACTAGC	4224
1801	QY	CGAAGTCTAGCTTGGCAAAACGACGGGTGGTATTCACATCCCAATCTTTGAATTTGGAG	1860
4225	Db	CGAAGTCTAGCTTGGCAAAACGACGGGTGGTATTCACATCCCAATCTTTGAATTTGGAG	4284
1861	QY	CGCATCATATTGGCAAAACGAATGAGATTTGTGATTAAGCAACAACCTGCTCTAAATACAT	1920
4285	Db	CGCATCATATTGGCAAAACGAATGAGATTTGTGATTAAGCAACAACCTGCTCTAAATACAT	4344
1921	QY	ATTCAAGGAATGTCAAGTCAATGGTCCCATAGTTCCTCATCTTTGGAAATTTCTATGGCA	1980
4345	Db	ATTCAAGGAATGTCAAGTCAATGGTCCCATAGTTCCTCATCTTTGGAAATTTCTATGGCA	4404
1981	QY	TTTCTCAATGGAAATGATCCGGATATATGGGATCCGTACAATGACAACTTTATCCCGTCC	2040
4405	Db	TTTCTCAATGGAAATGATCCGGATATATGGGATCCGTACAATGACAACTTTATCCCGTCC	4464
2041	QY	ACTACACTTTGAGAAATGTGTTGAAAGCAAGAGGGCTGCTAGAGGGCACTGCACGAGA	2100
4465	Db	ACTACACTTTGAGAAATGTGTTGAAAGCAAGAGGGCTGCTAGAGGGCACTGCACGAGA	4524
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4525	Db	AGTTTGGGTTACAGCAATCGATGCTCCCGTCTGAGGAATCGTCACTCGGCTGCACAGCCC	4584
2161	QY	AAAAGGGATCCACCTGATCAAGCATGCGATTCACCGTACACTCGAAACGGAAACGACAGG	2220
4585	Db	AAAAGGGATCCACCTGATCAAGCATGCGATTCACCGTACACTCGAAACGGAAACGACAGG	4644
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4645	Db	TGGTTTGTGTTTTCAGCGCGGCACTTCGAATCCAAAGTGTATTTTGTGTCAACTGGCGGA	4704
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all

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QY 2581 TGAACAGCGGATCTCAG 2598
Db 5005 TGAACAGCGGATCTCAG 5022

RESULT 4
AF023159 6027 bp mRNA linear PLN 18-APR-1998
LOCUS Zea mays starch synthase DULL1 (dull1) mRNA, complete cds.
DEFINITION
ACCESSION AF023159
VERSION AF023159.1 GI:3057119
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 6027)
Gao, M., Wanat, J., Stinard, P.S., James, M.G. and Myers, A.M.
Characterization of dull1, a maize gene coding for a novel starch
synthase
Plant Cell 10 (3), 399-412 (1998)
MEDLINE 98169346
PUBMED 9501113
2 (bases 1 to 6027)
Gao, M., James, M.G. and Myers, A.M.
Direct Submission
Submitted (06-SEP-1997) Biochemistry & Biophysics, Iowa State
University, 2152 Molecular Biology Building, Ames, IA 50011, USA
Location/Qualifiers
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be the maize starch synthase defined biochemically as
SSII"
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/protein_id="AAC14014.1"
/db_xref="GI:3057120"
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too late

ORIGIN

Query Match 100.0%; Score 2598; DB 8; Length 6027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 241 CATACAGAAATGAGCTTTGTGTTTTTAAACGACACACGGTATATGAAATATACAAATA 300
Db 2665 CATACAGAAATGAGCTTTGTGTTTTTAAACGACACACGGTATATGAAATATACAAATA 2724
QY 301 ATGATTCGTGATACAAATAGAAAGCACCATGGATGAAATTTTATTCAGGATTTCTTGG 360
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QY 361 CTGAAGAAAGCAACGAGAACTTCAGAAACCTTGCAAATGAGAAAGCTGAAAGGAGGAGAC 420
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Db 3025 TCAGATGCTTATTATACATAAACTCAAGACCTCTAGTTTCAAGTCTAGATATGATGTC 3084
QY 661 ATGGTGGCTATACAAATGAGATGATGAGTCTCTTTCTGCTGAAAGGCTTGTTCATCATC 720

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Qy	781		TGGACTGGGTTTTCTGACGGGCCACACGGAGGTGCAAGGAATTTATGACAAATGGAG	840
Db	3205		TGGACTGGGTTTTCTGACGGGCCACACGGAGGTGCAAGGAATTTATGACAAATGGAG	3264
Qy	841		GACATGATTTTCATGCTACCCCTTCCAAATAACATGACTGAGGAAGAGTATTTGGATGGAAG	900
Db	3265		GACATGATTTTCATGCTACCCCTTCCAAATAACATGACTGAGGAAGAGTATTTGGATGGAAG	3324
Qy	901		AAGAACAAAGGATCTATACAAGGCTTCAACAGAGAGGAGGGAAGAGGAGGCTATTATA	960
Db	3325		AAGAACAAAGGATCTATACAAGGCTTCAACAGAGAGGAGGGAAGAGGAGGCTATTATA	3384
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Qy	1021		TGTTCTGTGTTTCTCAGAAACAATTTGTATACACCGAACCACTTGAATAATCATGCTGGAA	1080
Db	3445		TGTTCTGTGTTTCTCAGAAACAATTTGTATACACCGAACCACTTGAATAATCATGCTGGAA	3504
Qy	1081		CTACTATTGATGTGCTTTATAATCTTCTAATACAGTTCATACTGGAAGCCAGAGTTT	1140
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Qy	1141		GGTTTCGATGTTCCCTTTAATCGTTGGATGTATCCAGGTGGGGTGTGCCACTCAGAAGA	1200
Db	3565		GGTTTCGATGTTCCCTTTAATCGTTGGATGTATCCAGGTGGGGTGTGCCACTCAGAAGA	3624
Qy	1201		TGCTACAAAGCAGAAAAATGGTTACACCTTAAAGCAACAGTTTACGTTCCAGAGATGCCT	1260
Db	3625		TGCTACAAAGCAGAAAAATGGTTACACCTTAAAGCAACAGTTTACGTTCCAGAGATGCCT	3684
Qy	1261		ATATGATGGACTTCGTTTTCTCGAGTTCAGAAAGGTGGAAATTTATGATTAACAGAAATG	1320
Db	3685		ATATGATGGACTTCGTTTTCTCGAGTTCAGAAAGGTGGAAATTTATGATTAACAGAAATG	3744
Qy	1321		GGTTAGACTATCATATTCCTGTTTTTGGGTCAAATTCGAAAGAAACCACTATGCATTG	1380
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Db	3805		TCCACATTTGCTTTCAGATGGCACCAATTCGCAAGGTTGGAGGTCTTGGTGTATGTTGCA	3864
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Db	3925		ACGGTTGCTTGAATCTAAGCAATGTCAGAAATCTACAAATCCATCAGAGTTTTCTTGGG	3984
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Qy	1621		AACCTCAAAATGGGATGTTTGGAGTCGGATATGATATGCGAGGGACGATGACCGCGAT	1680
Db	4045		AACCTCAAAATGGGATGTTTGGAGTCGGATATGATATGCGAGGGACGATGACCGCGAT	4104
Qy	1681		TTGGGTTCTTCTGTCCTTCTGTCTAGAGTTTCTCCTCCAAAGTGGATCTTCTCCGAACA	1740
Db	4105		TTGGGTTCTTCTGTCCTTCTGTCTAGAGTTTCTCCTCCAAAGTGGATCTTCTCCGAACA	4164
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Db	4225	CGAAGTCTAGCTTTGGCAAAACGACGGGTGGTATTCACCAATCCACAATCTTGAATTTGGAG	4284
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QY	1921	ATTCAAAGGAAGTGTTCAGGTCATGTGTGCCATAGTTCCCTCATCTTGGGAAATTTCTATGGCA	1980
Db	4345	ATTCAAAGGAAGTGTTCAGGTCATGTGTGCCATAGTTCCCTCATCTTGGGAAATTTCTATGGCA	4404
QY	1981	TTCTCAATGGAAATGATTCGGGATATATGGGATCCGTTACATGACAACTTTATCCCGTCC	2040
Db	4405	TTCTCAATGGAAATGATTCGGGATATATGGGATCCGTTACATGACAACTTTATCCCGTCC	4464
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QY	2161	AAAAGGGGATCCACCTGATCAAGCATCCGATTCACCGTACACTCGAAACGGAAACGACAGG	2220
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QY	2221	TGCTTTTGCTTTGCTTCAGCGCCCGGACTCTCGAATCCAAAGCTGATTTGTCTAAACCTGGCGA	2280
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QY	2281	ATACGCTCCACGGGCTPAAAACCATGGGCAAGTGAAGGCTTTCCCTGACCTACGACGAGCCTC	2340
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QY	2521	GCTTTGAGCCCAACGGGTTTACGTTTGTGCGGAGCTGTATAGCAACGGTGTGTGACTACGGCG	2580
Db	4945	GCTTTGAGCCCAACGGGTTTACGTTTGTGCGGAGCTGTATAGCAACGGTGTGTGACTACGGCG	5004
QY	2581	TGAACAGGGGAGTCTCAG	2598
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RESULT 5	AF258608	linear	PLN 27-JUL-2000
LOCUS	Triticum aestivum starch synthase III mRNA, complete cds.		
DEFINITION	AF258608	5346 bp	
ACCESSION	AF258608		
VERSION	AF258608.1		
KEYWORDS	GI:9502142		
SOURCE	Triticum aestivum (bread wheat)		
ORGANISM	Triticum aestivum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliopsida; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticeae; Triticum.		
REFERENCE	1 (bases 1 to 5346)		
AUTHORS	Li, Z., Mouille, G., Kosar-Hashemi, B., Rahman, S., Clarke, B.,		

Db 3453 CCTATATGATGACATTTGTTTCTCCGAGTGGAGAAATGGATCGATCTATGACAACAGCA 3512
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QY 2458 CTGGAGGGCTCTTCGACACTGTCTTCGATGTGGACAAATGACAAGGAACAGCCCGAGATC 2517
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QY 2578 CGCTGAACAGGGCGATC 2594
Db 4773 CCTCAACAGAGCAATC 4789

RESULT 6
AX653280
LOCUS AX653280
DEFINITION Sequence 3150 from Patent WO03000898.
ACCESSION AX653280
VERSION AX653280.1 GI:29156094
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katsirli, F., Quan, S., Tao, Y., Whitcham, S., Xie, Z., Zhu, F. and Zou, G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 3150 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES
source 1..5760
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ORIGIN
Query Match 65.6%; Score 1703.8; DB 6; Length 5760;
Best Local Similarity 79.2%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 497; Indels 42; Gaps 1;
1 AGCTTGCTGAAAAAATTTATTCGCTGGGAAACAAGTTGTTTACTTTATCCAGATGTTTGA 60
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3068	ATGCTGAAGAGCAGCAGCGAATGGAGAAACAAGGGCTGCAGAACAGCTGCCAGGGAAC	3127
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3128	AGGCTAAGACGAGATAGTTGAAGAGAAACAATAATTGCCAAATCTCTTGAGTTTACGCCA	3187
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3608	AAATAAGGTTGAGAAAGAGCAAAATGAAATCTGAGATGAAGGAAGAAGCTATGAGAA	3667
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1081	CTACTATTGATGTCTTTATAATCCCTCTAATACAGTTCTTAATGGAAGCCAGAGGTTT	1140
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4028	TCCATATAGCGGTTGAGATGGCAACCAATTGCAAAAGGTTGGAGGCTTGTCTGACGTTGTCA	4087
1441	CTAGTCTTTTCACTGCTGTGCAAGATTTAGGACAAATGTGGAGGTTATTCTTCCAAAGT	1500
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Tel:+81-29-838-7007, Fax:+81-29-838-7007)
 This clone is one of the 32k full-length cDNA clones from japonica rice.
 URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ozeki,H., Hotta,I., Kojima,K., Naniki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shisshiki,T., Yamamoto,M. and Nakahama,Y.
 FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kuroesaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,Y., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,K., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Ito,H., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Konda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ocar,Y., Saitoh,H., Sakai,C., Sakai,K., Sakai,K., Shibata,K., Sakagawa,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
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RESULT 8

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DEFINITION Sequence 4057 from Patent WO03000898.
ACCESSION AX654187
VERSION AX654187.1 GI:29157001
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, R. and Zou, G.
Plant genes involved in defense against pathogens
Patent: WO 0300898-A 4057 03-JAN-2003;
Syngenta Participations AG (CH)

FEATURES

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Location/Qualifiers
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ORIGIN

Query Match 63.4%; Score 1646.8; DB 6; Length 3645;
Best Local Similarity 77.1%; Pred.No. 0;
Matches 2002; Conservative 1; Mismatches 593; Indels 0; Gaps 0;

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QY 241 CATACAGATGGAATTTGTGTTTTTAAACGACACACGGGTATATGAAATATAACAATA 300
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VERSION AX755430.1 GI:32167798
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ORGANISM Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1
AUTHORS Zhu, T., Cheng, W., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,
Glazebrook, J., Katagiri, F., Kreps, J., Provart, N. and Rieke, D.
TITLE Identification and characterization of plant genes
JOURNAL Patent: WO 03000905-A 131 03-JAN-2003;
Syngenta Participations AG (CH)
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ORIGIN

Query Match 46.9%; Score 1217.6; DB 8; Length 3901;
Best Local Similarity 67.0%; Pred. No. 0;
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ACCESSION X95759.1
VERSION starch synthase.
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1
AUTHORS Marshall, J., Sidebottom, C., Debet, M., Martin, C., Smith, A.M. and
Edwards, A.
TITLE Identification of the major starch synthase in the soluble fraction
of potato tubers
JOURNAL Plant Cell 8 (7), 1121-1135 (1996)
MEDLINE 96305754
PUBMED 8768372
REFERENCE 2 (bases 1 to 4127)
AUTHORS Edwards, A.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-1996) A. Edwards, John Innes Centre, Colney Lane,
Norwich, Norfolk NR4 7UH, UK
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ORIGIN

Query Match 46.4%; Score 1206.4; DB 8; Length 4127;
Best Local Similarity 66.8%; Pred. No. 0;
Matches 1736; Conservative 0; Mismatches 861; Indels 3; Gaps 1;

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STSSIII		
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ACCESSION	X94400	PLN 16-APR-1999
VERSION	X94400.1	
KEYWORDS	soluble starch synthase; SSSI gene.	
SOURCE	Solanum tuberosum (potato)	
ORGANISM	Solanum tuberosum	
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REFERENCE	1	
AUTHORS	Abel, G.J., Springer, F., Willmitzer, L. and Kosmann, J.	
TITLE	Cloning and functional analysis of a cDNA encoding a novel 139 kDa starch synthase from potato (Solanum tuberosum L.)	
JOURNAL	Plant J. 10 (6), 981-991 (1996)	
MEDLINE	97164391	
PUBMED	9011082	
REFERENCE	2 (bases 1 to 4167)	
AUTHORS	Abel, G.J.W.	
TITLE	Direct Submission	

ORIGIN	Query Match	46.4%;	Score 1204.8;	DB 8;	Length 4167;
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Db	1235	ACCTGATGAAGATGTCGAGATATTTCTTAACAGAGGTCTTTCACCTTTGAAGAATGAGTC	1294		
Qy	122	TGATGTACTTATCAAGCGAGCATTCAATGGGTGGAAGTGGAGATTTTCTACTGAAAAAAT	181		
Db	1295	TGATGCTTGATTATGGAGCTTTTATGATGTTGGCGCTATAGGTCTTTTACTACAAGCT	1354		
Qy	182	GCACAGAGCGAGCTGCGAGGGAGCTGGTGGTCTGCAAACTATACATTCCTTAAGCAGGC	241		
Db	1355	AACGTGAGACTCATCTCAATGGAGATGGTGGTCTTGAAGATCCATGTTCCCAAGGAAGC	1414		
Qy	242	ATACAGAAATGGACTTGTGTGTTTTTAAACGGACACACGCTATATGAAAATTAATACAAATAA	301		
Db	1415	ATACAGGGCTGATTTTGTTTTTTAATGACACAGATGCTATGACACAAATGATGGAAA	1474		
Qy	302	TGATTTTCGTATACAAATAGAAAGCACCATGGATGAAAAATTTATTTGAGGATTTCTTGGC	361		
Db	1475	TGACTTCAGTATAACTGTGAAAGGTGGTATGCAAAATCATTGACTTTGAAAATTTCTTGCT	1534		
Qy	362	TGAAGAAAAACCAACGAGAACCTTGAGAACCTTTGCAAACTGAGGAAGCTGAAAGGAGGACA	421		

1535	TGAGGAAATGGAGAGAACGAGAGAAACTTGCTGCTAAAGAAACAAGCTGAAAGAGAAAGACT	1599
422	AACTGATGACGACGCGGAATGGAGGAAGAAAGGGCCGACGATAAAGCTGCACGGGTACA	481
1595	AGCGGAAGAACAAAGACGAAATAGNAGCAGAGAAAGCTGAAATTTGAAGCTGCACAGAGCAC	1654
482	AGCCAGGTTGAGGTAGACGACGAGAGAGAAATAAATTTGTGCAATGTATTGGTTTGGCTTACCCAG	541
1655	AGCAAGGAAGAGGCTGCAAGAGAAAGAAAGATTTGCGAGAAATGATGTGTAAGAGCCAC	1714
542	AGCTCCTGTTTGATAATTTATGTGTACATTTGAGCCCATCAAGACTGGGACAAAGAGGCTACTGT	601
1715	GAAGACTCGTGATACACGTGGTACATAGAGCCAAAGTGAATTTAAATGCGAGGACAAGGT	1774
602	CAGATTGTATTAAACAATAAACTCAAGACCTCTAGTTTCA CAGTACTGAGATATGGGATGCA	661
1775	CAGGTTATACTAAACAAAGTTTCAGTGCTCTCTCCCATGCTTAAGGACCTGTGGATCCA	1834
662	TGTTGCTATAACAAATGGATTCATGACCTCTCTTTTGTGTAAGAGGCTTCTTCATATCA	721
1835	CGAGAGATATAAATTTGGNAGATGGTTTGTCTATTGTCAAAAGCTTGTTAAATCTGA	1894
722	TGACAAAGATTGGAATGGTGGTTTCAGATGTTGTGTCCTGCAAGAAACAATATGTAAT	781
1895	GAGATAGATGGTGCAATTTGGTGGTATACAGAGGTGTGTTATTCCTGATCAGGCACCTTTCTT	1954
782	GGACTGGGTTTTGCTGACGGCCCCACAGGAGCTGCAAGGAATTTATGACAACTATGGAGG	841
1955	GGATGGGTTTTGCTGATGGTCCACCCAAAGCATGCCATTTGCTTTATGTAACAACTACCG	2014
842	ACATGATTTTCATGCTACCCCTTCCAAATACATGACTGAGGAAAGATTTGGATGGAAAGA	901
2015	CCAAGACTTCCATGCCATTGTGCCCAACACATTCGGAGGAAATTAATTGGGTGGAGGA	2074
902	AGAACAAAGATCTATCAGAGCTTCAACAGAGAGGAGGAAAGGAGAGGCTATTAA	961
2075	AGAACAACAGATCTTTAAGACACTTCAGGAGGAGAGAGGCTTAGAAGACGGCTATGCG	2134
962	AAGCAAGGCTGAGAGAAATCAAAATATGAAAGCTGAGATGAAGGAAAGACTATGAGAAAT	1021
2135	TGCTAGGTTGAAAACACAGCACTTCTGAAAACCTGAAACAAAGGAAAGAACTATGAATC	2194
1022	GTTCCTGGTTTTCAGAAACACATTTGTTTACACGAAACCACTTGGAATAATGCTGGAAC	1081
2195	ATTTTTACTGCTCAGAAAGCATGTAGTATATATCTGAGCCTCTTGATATCCAAGCTGGAAG	2254
1082	TACTATTGATGTGCTTTATAATCCTTCTAATACAGTTTCTAACTGGAAGCCAGAGGTTTG	1141
2255	CAGGTCACAGTTTACTATTAATCCGCGCAATACAGTACTTAATGGTAAAACCTGAAATTTG	2314
1142	GTTCGATGTTCTTTAATCGTTGGATGTATCCAGGTGGGGTGTGCCACTCAGAAGAT	1201
2315	GTTCAGATGTTCAATTAATCGCTGGACTCACCGCTGGGTCATTTGCACTCCTCAGAAAAAT	2374
1202	GGTACAGCAGAAAATGGTTTCACTTAAGCAACAAGTTTACGTTCCACGAGATGCTTA	1261
2375	GTCCCTGCTGAAAATGGCAACCATGTCCAGAACACTGTGAAGGTTCCATTGGATGATA	2434
1262	TATGATGGACTTCGTTTTCTCGGAGTCAGAAAGAGGTGGAATTTATGATAACAGAAAATGG	1321
2435	TATGATGATTTTGTATTTTCCGAGAGAGAAGATGGTGGGATTTTTCACAAATAAGAGCGG	2494
1322	GTTAGACTATCATATTCTCTGTTTTTTGGGTCAAATTCGAAAGGAACCACTATGCATTTGT	1381
2495	AATGGACTATCACATACCTGTGTTTGGAGAGGTGCTTAAGAAACCTCCAATGCATATTGT	2554
1382	CCACATTGCTGTTGAGATGGCACCAATCGCAAGGTTTGGAGGCTCTTGCTGATGTTGTAC	1441
2555	CCATATTGCTGTGAATATGSCACCAATTCGAAAGTGGGAGGCTTGCTGATGTTGTATC	2614
1442	TAGTCTTTACGTCCTGTGCAAGATTTAGGACACAAATGTCGAGGTTTATCTTCCAAAGTA	1501
2615	TAGTCTTTCCCGTGTGTTTCAAGATTTAAACCAATAATGTGGATATTATCTTACCTAAGTA	2674

QY	1502	CGGTTGCTTGAATCTNAGCAATGTCAAGAAATCTA	2579	GCTGAACAGGGCGGATCTCAG	2598
Db	2675	TGACTGTTTGAAGATGAATAATGTGAAGGACTTTC			
QY	1562	TGGTTCTGAAATAAATGTGTGGCGTGCAGTCTAGT	3755	TCAGAAATAGAGCTCTCTCTG	3774
Db	2735	TGGGACTGAAATAAAGATATGGTTGGAAAGGTGGA			
QY	1622	ACCTCAAAATGGGATGTTTGGAGTCGGATATGATAT			
Db	2795	GCCTCAAAACGGGTTATTTTCGAAAGGGTGGCTAT			
QY	1679	ATTGGCTTCTTCTGCTGCTCTAGAGTTTCTCCTCCA			
Db	2855	ATTGGTGTCTTCTGTCACGGGCTTTGGAGTTTCTT			
QY	1739	CATAATACATTTGCCATGATTGGTCAAGTGTCTCT			
Db	2915	TATCATTTCAATGGCCATGATTTGGTCTAGTGTCT			
QY	1799	CGGAAAGTCTAGCTTGGCAAAACGACGGGTGGTATT			
Db	2975	TACACACTATGGTCTAAGCAAACTCGTATAGTCTT			
QY	1859	AGGCATCATATTGGCAAGCAATGAGATATTGTGATA			
Db	3035	GGCAGATCTCAATTTGGGAGAGCAATGACTAACCG			
QY	1919	ATATTCAAAAGGAAGTCTCAGGTGATGTCATGTCAT			
Db	3095	TTACTCACAGGAGGTGCTTGGAAACCCCTGTAATT			
QY	1979	CAATCTCAATGGAATTTGATCCGGATATATGGGAT			
Db	3155	TATAGTGAATGGGATTTGACCCAGATATTTGGGAT			
QY	2039	CCACTACACTGTGAGAACTGTGTTGAAGCAAGAGG			
Db	3215	TCCGTACACTCTAGAAACCGTTTGAAGGCAAAAC			
QY	2099	GAAGTTTGGGTTACAGCAAAATCGATGTCCCGCTG			
Db	3275	AAAACTTGGACTGAACAGGCTGACCTTCTCTTGGT			
QY	2159	CGAAAGGGGATCCACTGATCAAGCATGCGATTCAC			
Db	3335	CCAGAAAGGAATCCACTCAATTAACATGCTATTTG			
QY	2219	GGTGGTTTGTGTTTGGTTCAGCGCGGACTCTCGAA			
Db	3395	GGTAGTCTTGTCTTGGTTCTGCTCTGATCTCTAGG			
QY	2279	GAAATAGCTTCCACGGGTTAAACCATGGGCAAGT			
Db	3455	AAATCAATTGCACTCCAAATATTAATGACCGCGC			
QY	2339	TCCTCGCATCTGATATACGCTGGCTCTGACTTCA			
Db	3515	ACTTCTCAGCTGATATATGCTGGTGTGATTTTATT			
QY	2399	TTGGGCTTAACCTCAGCTCGCTCGCATGCGGTAT			
Db	3575	ATGTGGACTTAACAACTTACCGCTATGAGATATGG			
QY	2459	TGGAGGGCTCTTCGACACTGTCTTTCGATGTGGCA			
Db	3635	TGGAGGACTTTATGATACTGTAATTTGATGTGACC			
QY	2519	AGGCTTTGAGCCCAACGGGTTTACGTTTGGAGCTG			
Db	3695	TGGTCTTGAACCAAAATGGATTCAGCTTTGATGGAG			

Search completed: June 20, 2004, 10:07:31
Job time : 16055 secs

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 01:59:08 ; Search time 1450 Seconds

(without alignments)

7611.599 Million cell updates/sec

Title: US-10-634-262-1_COPY_2425_5022

Perfect score: 2598

Sequence: 1 agctgtcgtaaaattat.....gctgaacaggcgatctcag 2598

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseqn 29Jan04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002s:*

7: geneseqn2003as:*

8: geneseqn2003bs:*

9: geneseqn2003cs:*

10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2598	100.0	6027	2 AAX58751	Aax58751 Maize dul
2	2598	100.0	6027	7 ABX09935	Abx09935 DNA encod
3	1766.6	68.0	5346	3 AAC86413	Aac86413 Wheat sta
4	1744.2	67.1	3621	3 AAC86414	Aac86414 Wheat sta
5	1703.8	65.6	5760	7 ADAC69827	Ada69827 Rice gene
6	1646.8	63.4	3645	7 ADA70734	Ada70734 Rice gene
7	1581.4	60.9	3032	9 ADC07865	Adc07865 Rice DNA
8	1500.4	57.8	4121	5 AAF61270	Aaf61270 Maize sta
9	1204.8	46.4	4127	2 AAT68646	Aat68646 Potato so
10	1141.2	43.9	3078	7 ADA68321	Ada68321 Arabidops
11	931	35.8	2301	2 AAT32324	Aat32324 Soluble s
12	501	19.3	2446	3 AAC86416	Aac86416 Wheat sta
13	501	19.3	11611	3 AAC86432	Aac86432 Wheat SSI
14	290.6	11.2	548	6 AAD33325	Aad33325 Rice star
15	207.6	8.0	437	6 AAD33324	Aad33324 Rice star
16	197.6	7.6	1032	3 AAC86417	Aac86417 Wheat sta
17	183.8	7.1	297	6 ABL73972	Ab173972 Corn tass
18	176.4	6.8	299	6 ABL74146	Ab174146 Corn tass
19	175	6.7	212	7 ABX81641	Abx81641 Corn ear
20	145	5.6	2652	2 AAT75137	Aat75137 DNA encod
21	145	5.6	3430	9 AAD60671	Aad60671 Corn star
22	144.8	5.6	3434	6 ABS52829	Abs52829 Maranta a
23	140.8	5.4	1275	4 AAS00044	Aas00044 Wheat CDN

24	140.8	5.4	1275	9 AAD60675	Aad60675 Wheat sta
25	140.8	5.4	3386	9 AAD60676	Aad60676 Wheat sta
26	140.4	5.4	1592	3 AAC86420	Aac86420 Wheat sta
27	137.6	5.3	759	9 ADC08765	Adc08765 Wheat DNA
28	136.2	5.2	240	6 ABL73926	Ab173926 Corn tass
29	134.4	5.2	3453	9 AAD60673	Aad60673 Rice star
30	133	5.1	871	3 AAC86419	Aac86419 Wheat sta
31	125.2	4.8	2865	7 ADA70571	Ada70571 Rice gene
32	122.4	4.7	892	3 AAC86418	Aac86418 Wheat sta
33	112.4	4.3	165	9 ADC08820	Adc08820 Corn DNA
34	111.8	4.3	2380	2 AAV66834	Aav66834 Zea mays
35	110.8	4.3	2478	2 AAT67287	Aat67287 Soluble s
36	110.2	4.2	2622	7 ADA69445	Ada69445 Rice gene
37	106.8	4.1	579	9 ADC08619	Adc08619 Banana DN
38	92.2	3.5	2115	3 AAC32824	Aac32824 Arabidops
39	87	3.3	2179	7 ABQ80055	Abq80055 Soybean g
40	86.8	3.3	2423	2 AAV70958	Aav70958 DNA encod
41	85.6	3.3	2097	2 AAV29755	Aav29755 Zea mays
42	85.6	3.3	2480	7 ABX09934	Abx09934 DNA encod
43	79.6	3.1	1984	3 AAC46797	Aac46797 Arabidops
44	77.4	3.0	2202	6 ABS52823	Abs52823 Curcuma z
45	76	2.9	2946	6 ABK88115	Abk88115 cDNA enco

ALIGNMENTS

RESULT 1

AAX58751

ID AAX58751 standard; cDNA; 6027 BP.

XX AAX58751;

XX DT 16-AUG-1999 (first entry)

XX DE Maize dull1 gene encoding starch synthase enzyme DUL.

XX KW Starch synthase; SSII; DUL; dull1 gene; maize; transgenic plant; ss.

XX OS Zea mays.

XX FH Key Location/Qualifiers

FT misc_feature 1..1437

FT /tag= f

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 16"

FT CDS 120..5147

FT misc_feature /tag= a

FT /tag= b

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 12"

FT misc_feature 565..816

FT /tag= d

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 14"

FT misc_feature 655..1221

FT /tag= c

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 13"

FT misc_feature 1369..1944

FT /tag= e

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 15"

FT misc_feature 1438..2424

FT /tag= g

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 17"

FT misc_feature 2425..3791

FT /tag= h

FT /note= "functional fragment of cDNA specifically claimed

FT in Claim 18"

XX

QY	1501	ACGGTTCGTTGAAATCTAAGCAATGTCTCAAGAAATCTACAAATCCATCAGAGTTTCTCTGGG	1566
Db	3925	ACGGTTCGTTGAAATCTAAGCAATGTCTCAAGAAATCTACAAATCCATCAGAGTTTCTCTGGG	3984
QY	1561	GTGGTTCTGAAATAAATGTGTGGCGTGGACTAGTCGAAAGGCCCTTGTGTATTACTTCTCTGG	1620
Db	3985	GTGGTTCTGAAATAAATGTGTGGCGTGGACTAGTCGAAAGGCCCTTGTGTATTACTTCTCTGG	4044
QY	1621	AACTCTCAAAATGGGATGCTTTTGGAGTCGGATATGTATATGGCAGGGACGATGACCGCGCAT	1680
Db	4045	AACTCTCAAAATGGGATGCTTTTGGAGTCGGATATGTATATGGCAGGGACGATGACCGCGCAT	4104
QY	1681	TTGGCTTCTTCTGTGCTCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCGGAACA	1740
Db	4105	TTGGCTTCTTCTGTGCTCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCGGAACA	4164
QY	1741	TAATACATTTGCCATGATTGTCTCAAGTGCTCCTGTGTGCTCGCTGGCTACACAAGGAAAACTACG	1800
Db	4165	TAATACATTTGCCATGATTGTGTCAAGTGCTCCTGTGTGCTCGCTGGCTACACAAGGAAAACTACG	4224
QY	1801	CGAAGTCTAGCTTGGCAAACGACCGGTGGTATTACCACTCCAAATCTTTGAAATTTGGAG	1860
Db	4225	CGAAGTCTAGCTTGGCAAACGACCGGTGGTATTACCACTCCAAATCTTTGAAATTTGGAG	4284
QY	1861	CGCATCATATTGGCAAAACGAATGAGATATTGTGTATAAAGCAAACAACTGTCTCTAATAAT	1920
Db	4285	CGCATCATATTGGCAAAACGAATGAGATATTGTGTATAAAGCAAACAACTGTCTCTAATAAT	4344
QY	1921	ATTCAAAGGAAGTCTAGGTCATGGTGCCATAGTTCTCTCATCTTGGGAAATTTCTATGGCA	1980
Db	4345	ATTCAAAGGAAGTCTAGGTCATGGTGCCATAGTTCTCTCATCTTGGGAAATTTCTATGGCA	4404
QY	1981	TTCTCAATGGAATTTGATCCGGATATATGGGATCGGTACAACTTGAACTTATCCCGGTCC	2040
Db	4405	TTCTCAATGGAATTTGATCCGGATATATGGGATCGGTACAACTTGAACTTATCCCGGTCC	4464
QY	2041	ACTACACTTGTGAGAAATGTGGTTGAAGGCAAGAGGGCTGTCTAAGAGGGCACTGCAGCAGA	2100
Db	4465	ACTACACTTGTGAGAAATGTGGTTGAAGGCAAGAGGGCTGTCTAAGAGGGCACTGCAGCAGA	4524
QY	2101	AGTTTGGTTTACAGCAAAATCGATGTCCTCCGTCGTAGGAAATCGTCACTCGCCTGACAGCCC	2160
Db	4525	AGTTTGGTTTACAGCAAAATCGATGTCCTCCGTCGTAGGAAATCGTCACTCGCCTGACAGCCC	4584
QY	2161	AAAAGGGATCCACCTGATCAAGCATGCGATTCTCACCGTACACTCGAACGGAAACGGACAGG	2220
Db	4585	AAAAGGGATCCACCTGATCAAGCATGCGATTCTCACCGTACACTCGAACGGAAACGGACAGG	4644
QY	2221	TGTTTGTGTTGTTCAGCGCCGGACTCTCGAATCCAAAGTGTATTTTGTCTCAACTGCGCA	2280
Db	4645	TGTTTGTGTTGTTCAGCGCCGGACTCTCGAATCCAAAGTGTATTTTGTCTCAACTGCGCA	4704
QY	2281	ATACGCTCCACGGGTAAACCAATGGGCAAGTGAGGCCTTCTTGACCTTACGACGAGCCTC	2340
Db	4705	ATACGCTCCACGGGTAAACCAATGGGCAAGTGAGGCCTTCTTGACCTTACGACGAGCCTC	4764
QY	2341	TCTCGCATCTGATATACGCTGGCTCTGACTTCACTTCTGGTCCCATCTATATTTTGTAGCCTT	2400
Db	4765	TCTCGCATCTGATATACGCTGGCTCTGACTTCACTTCTGGTCCCATCTATATTTTGTAGCCTT	4824
QY	2401	CGCGCCTTAACCTAGCTCGTGCCCAATGGGAACCAATCCCGATTTGTCCGCAAGACTG	2460
Db	4825	CGCGCCTTAACCTAGCTCGTGCCCAATGGGAACCAATCCCGATTTGTCCGCAAGACTG	4884
QY	2461	GAGGGCTTTCGACACTGTCTTCGATGTGGCAATGACAAGGAACGAGCCCGAGATCGAG	2520
Db	4885	GAGGGCTTTCGACACTGTCTTCGATGTGGCAATGACAAGGAACGAGCCCGAGATCGAG	4944
QY	2521	GCCTTTGAGCCCAAACGGGTTTACGTTTGTGACGAGCTGTATAGCAACCGGTGTTGACTACGCGC	2580
Db	4945	GCCTTTGAGCCCAAACGGGTTTACGTTTGTGACGAGCTGTATAGCAACCGGTGTTGACTACGCGC	5004
QY	2581	TGAACAGGGCGATCTCAG	2598

Db 5005 TGAACAGGGCGGTCTCAG 5022
 |||||
 RESULT 2
 ABX09935
 ID ABX09935 standard; DNA; 6027 BP.
 XX
 XX AC ABX09935;
 XX
 XX 17-FEB-2003 (first entry)
 XX
 XX DNA encoding maize Starch synthase III (Dul).
 XX
 XX Starch; starch synthase; glucan association domain; GLASS; linker domain;
 XX KW LINKR; glucosyl transferase domain; GLYTR; C-terminal end; CTEND;
 XX KW granule bound starch synthase; GBSS; morphology; retrogradation;
 XX KW waterbinding; swelling potential; gene; ds.
 XX
 XX Zea mays.
 XX
 XX W0200279410-A2.
 XX
 XX 10-OCT-2002
 XX
 XX 29-MAR-2002; 2002WO-US009574.
 XX
 XX 30-MAR-2001; 2001US-0279720P.
 XX
 XX (BADI) BASF PLANT SCI GMBH.
 XX
 XX Commuri P, Keeling PL, Ramirez N, Mckean A, Gao Z, Guan H;
 XX WPI; 2003-040678/03.
 XX
 XX New DNA encoding fusion protein consisting of 4 different functional
 XX PT domains selected from glucan association domain, linker domain, glucosyl
 XX PT transferase domain, and C-terminal end, useful for producing modified
 XX PT starches.
 XX
 XX Claim 33; Page 225-227; 265pp; English.
 XX
 XX The invention describes an isolated DNA molecule encoding a fusion
 XX CC protein consisting of 4 different functional domains selected from glucan
 XX CC association domain (GLASS), linker domain (LINKR), glucosyl transferase
 XX CC domain (GLYTR), and C-terminal end (CTEND) which are operably linked to
 XX CC one another. The DNA molecule is useful for expressing in plants
 XX CC polypeptides including starch synthase enzymes as fusion proteins with
 XX CC improved affinity to starch and modified catalytic capabilities and to
 XX CC the in vivo and in vitro synthesis of glucan chains of modified lengths
 XX CC as compared to plants producing native starch or starch produced with
 XX CC native starch synthases. Expression of the starch synthase fusion
 XX CC proteins along with granule bound starch synthase (GBSS) will lead to a
 XX CC modified starch having an altered or improved morphology, retrogradation,
 XX CC waterbinding, or swelling potential of the granules, gel strength,
 XX CC adhesiveness, cohesiveness, hardness, elasticity, increased or decreased
 XX CC granule size, degree of branching, crystallinity, degree of cross-
 XX CC linking, and increased or decreased glucan chain lengths. This sequence
 XX CC encodes a starch synthase used in the invention
 XX
 XX SQ Sequence 6027 BP; 1800 A; 1177 C; 1441 G; 1609 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 2598; DB 7; Length 6027;
 XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 AGCTTGCTGAAAAAATATTGCGTGGGAAACAAGTTGTTTACTTATCCAGATGTTATGA 60
 Db 2425 AGCTTGCTGAAAAAATATTGCGTGGGAAACAAGTTGTTTACTTATCCAGATGTTATGA 2484
 Qy 61 AAGCTGATTCAACAAATTGATCTCTATTTCATCGTGAATCTATCAGCTGTGCCAATGAGC 120
 Db 2485 AAGCTGATTCAACAAATTGATCTCTATTTCATCGTGAATCTATCAGCTGTGCCAATGAGC 2544

Db 4705 ATACGCTCCACGGGTAACCACTGGGCACTGAGGCTTTCCTTGACCTACGAGGCTC 4764
Qy 2341 TCTCGCATCTGATATACGCTGGCTCTGACTTCACTCTGGTCCCATCTATATTTGAGCCTT 2400
Db 4765 TCTCGCATCTGATATACGCTGGCTCTGACTTCACTCTGGTCCCATCTATATTTGAGCCTT 4824
Qy 2401 GCGGCTTAACCTCAGCTGCTGCGCATGCGGTATGGAACCATCCCGATTGTCGCAAGACTG 2460
Db 4825 GCGGCTTAACCTCAGCTGCTGCGCATGCGGTATGGAACCATCCCGATTGTCGCAAGACTG 4884
Qy 2461 GAGGCTCTTTCGACACTGCTCTTCGATGTGACAAATGACAAGGAACGAGCCCGAGATCGAG 2520
Db 4885 GAGGCTCTTTCGACACTGCTCTTCGATGTGACAAATGACAAGGAACGAGCCCGAGATCGAG 4944
Qy 2521 GCCTTGAGCCCAACGGGTTTAGCTTTGACGAGCTGATGCAACGGTGTGACTACGCGC 2580
Db 4945 GCCTTGAGCCCAACGGGTTTAGCTTTGACGAGCTGATGCAACGGTGTGACTACGCGC 5004
Qy 2581 TGAACAGGGGCTCTCAG 2598
Db 5005 TGAACAGGGGCTCTCAG 5022

RESULT 3
AAC86413
ID AAC86413 standard; cdna; 5346 BP.
AC AAC86413;
XX
DT 01-MAR-2001 (first entry)
DE Wheat starch synthase III coding sequence SEQ ID NO: 7.
XX
KW Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
KW food product; adhesive; ss.
XX
OS Triticum aestivum.
XX
PN W0200066745-A1.
XX
PD 09-NOV-2000.
PF 28-APR-2000; 2000WO-AU000385.
XX
PR 29-APR-1999; 99AU-00000052.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
PI Morell M, Li Z, Rahman S, Appels R;
XX
XX WPI; 2000-647602/62.
DR P-PSDB; AAB37569.
XX
PT Nucleic acid molecules encoding wheat starch synthase (wst)-I and wst-II,
XX useful in modifying plant starch content and/or composition.
PS Claim 1; Page 165-172; 21lpp; English.
XX
CC The present invention relates to novel protein and coding sequences from
CC wheat. The proteins are wheat starch synthases, designated SSII and
CC SSIII. These can be used in the modification of plant starch content or
CC composition, and to screen plants to identify mutations which affect
CC starch content and composition. The starch can then be used in food
CC products, such as flour, and in films, coatings, adhesives, building
CC materials and packaging materials
XX
SQ Sequence 5346 BP; 1601 A; 994 C; 1378 G; 1373 T; 0 U; 0 Other;

Query Match

68.0%; Score 1766.6; DB 3; Length 5346;

Best Local Similarity

80.3%; Pred. No. 0;

Matches 2085; Conservative 0; Mismatches 509; Indels 3; Gaps 1;
Qy 1 AGCTTCTGAAAAAATTTATTCCTGGGAAAACAAGTTGTTTCTTATCCAGATGTATTGA 60
Db 2193 AACTCCTGAGAAAAAATTTATTCGATGAGAAACAAGCTGTTGTTGTTTCCAGAGGTAGTGA 2252
Qy 61 AAGCTGATTCAACAATTTGATCTCTATTTCAATCGTGTATCATCAGCTGTGCCCAATGAGC 120
Db 2253 AAGCTGATTCAAGTTATGATCTCTATTTAAATCGTGAACCTTACAGCTTTGGCGAATGAAC 2312
Qy 121 CTGATCTACTTATCAAAGGAGCAATTCAATGGGTGGAAGTGGAGATTTTTCACCTGAAAAAT 180
Db 2313 CCGATGTCGTTCATCAAAGGAGCAATTCAATGGGTGGAAGTGGAGCTTTTTCACCTGAAAAAT 2372
Qy 181 TGCACAAGAGCGAGCTGGCAGGGGACTGTGTGGTGTGCAAACTATACATTCCTTAAGCAGG 240
Db 2373 TGCACAAGAGCTGACCTTGGAGGGGTTTGGTGTGTTTGCAAAACCTGTACATCCCAAGGAGG 2432
Qy 241 CATACAGAAATGGACTTTGTGTTTAAACGACACACGCGTATATGAAAATAAATAACAATA 300
Db 2433 CCTACAGATTAGACTTTGTGTTCTTCAAAGTGGCGCGTCTATGAGAACAAATGGGCAACA 2492
Qy 301 ATGATTTCTGTATACAAATAGAAAGCACCATGATGAAATTTTATTGAGGATTTCTTGG 360
Db 2493 ATGATTTCTGTATAGGAATAGAAAGGCATATGAATGAAGATCTGTTTGAAGTTTCTTGG 2552
Qy 361 CTGAAGAAAGCAACGAGAACTTTGAGAACTTCCAAATGAGGAAGCTGAAAGAGGAGAC 420
Db 2553 TTAAGAAAGCAACGAGGAGCTTTGAGAACTTCCCAATGGGAAGAGCTGAAAGAGGAGCAC 2612
Qy 421 AAACCTGATGAGCAGCGCGCAATGGAGGAAGAAAGCGCGCAGATATAAGCTGACAGGGTAC 480
Db 2613 AGACTGAGAAACAGCGCGGAGAAAGAAAGCAAGGCTGCGAGATGAAGCTGTAGGGCAC 2672
Qy 481 AAGCCAAAGTTGAGGTAGAGACGAAGAATAAATTTGTGCAATGTATTGGGTTTAGCCA 540
Db 2673 AAGCGAAAGCGCGAGATAGAGATCAAGAAGAAAAAATTTGCAAGTATGTTGAGTTGSCCA 2732
Qy 541 GAGCTCCTGTTGATTAATTTATGATACATTTGATGAGCCCATCAGACTGGACAGAGCTACTG 600
Db 2733 GAAATGTTGATTAATTTGTTGTTGATAGAGCTAGCAGATACAAAGAGGAGATACTA 2792
Qy 601 TCAGATTGATTATAACATAAACTCAAGACCTCTAGTTACAGTACTGACATATGATGTC 660
Db 2793 TCAGTTTATTTATACAGAACTTCGAGGCCACTTGGCATATGACTGAGATTTGGATGC 2852
Qy 661 ATGGTGGCTATAACAATTTGATTTGATGAGCTCTCTTTTGTCTGAAAGCTTTGTCAATC 720
Db 2853 ATGGTGGTTACAACAATTTGACAGATGAGCTCTCTATTTGTTGAAAGCTTTGTCAAGTGA 2912
Qy 721 ATGACAAAGATTCTGATTTGGTGGTTTGCAGATGTTTGTGCTGCTGAAAGACATATGAT 780
Db 2913 ATGACAAAGACGGCGATTGGTGGTATGCGATGTTTATTCACCTGAAAGGCACTTGTGT 2972
Qy 781 TGGACTGGGTTTTTGTGTCAGCGCCCAAGGAGTGCAGGAAATTTATGACAAATGAGAG 840
Db 2973 TGGACTGGGTTTTTGTGTCAGCGCGCAGCTGGGAATGCNAGGAATGACAAATGCTC 3032
Qy 841 GACATGATTTTCATGCTACCCCTTCCAAATAACA---TGAAGTGGAGAGTATTTGGATGG 897
Db 3033 GACATGATTTTCCATGCTATTTCTTCCGAACAACAATGTAACCGAGGAAGGCTTCTGGCGCG 3092
Qy 898 AAGAAGCAACAAAGGATCTATACAGGCTTCAACAGAGAGGAGGGAAGGAGGAGGCTA 957
Db 3093 AAGAGAGCAAAACATCTATACAGGCTTCTGCAAGAAAGAGGAGAAAGGAGAAACCA 3152
Qy 958 TTAAGAGGAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAAGAAAACACTATGA 1017
Db 3153 TGAAGAGAGGCTGAGAGAAATGCAAAATGCAAAATGCAAGCTGAGTCAAGGCAAAACTATGC 3212
Qy 1018 GAATGTTCTGTTTCTCGAAACAATTTGTTTACCGGAACCACTTGAATAATCATGCTG 1077
Db 3213 GAAGGTTTCTGCTTTCCCGAAACACATTTGTTTATACCGAACCGCTTGAATAATCGTGCG 3272

1078 GAACCTACTATGATGCTTTATTAATCCCTTCTTAATAACAGTCTTAACCTGGAAGCCAGAGG 1137
1138 TTTCGGTTTCAGATGTTCCCTTTAATCGTTGGATGATCCAGGTGGGGTGTGTGCACCTCAGA 1197
1333 GTTGGTTTGAATGCTCCTTTAACTTTGGATGCAATCAAGTGGGGCAATGCCACCCAGA 3392
1198 AGATGGTACAGACAGAAATGGTTTCAACCTTAAAGCAACAGTTTACGTTCCACAGATG 1257
1393 AGATGGTGAATCAGGGGATGGCGGCTCTTAAAGCAACAGTTTGAATGTTCCACCGGATG 3452
1258 CCTATATGATGACTTCTGTTTCTCGAGTCAAGAGAGGTGGAAATTTATGATTAACAGAA 1317
1353 CCTATATGATGACTTCTGTTTCTCGAGTGGGAGAGATGGGATCTATGACAAACAGGA 3512
1318 ATGGGTTAGACTATCATATTCCTGTTTCTGGGTCAATTTGCAAGCAACCACTTATGCACA 1377
1353 ATGGGATGGAATCAATATTCCTGTTTCTGATTCATTTGAACAGAGAAATTTACATGCGTA 3572
1378 TTGTCCACTTGTCTGATGAGTGCACCAATCGCAAGTTTGGAGGTTTGGTGAATGTTG 1437
1353 TTATCCACTTGTGAGATGGCGGCTTGAAGGTTTGGAGGTTTGGGATGTTG 3632
1438 TCACCTAGTCTTTCAGTCTGTCGAAGATTTAGACACAAATGTCGAGGTTTATCTTCCAA 1497
1353 TTACAGGCTTCTTCAAGTCCCAATCAAGATCTAGGACATCTGTCGAGGTTTATCTCCCGA 3692
1498 AGTACGGTTGCTTGAATCTAAGCAATGTCAAGAAATCTACAAATCCATCAGAGTTTCTT 1557
1353 AGTACGACTGTTTGAACCAAGCAAGTGTCAAGGATTTACATTTATATCAAAAGTTTCTT 3752
1558 GGGGTGTTCTGAATAAATGTTGGCGTGAATGTCGAAGGCTTTGTGTTACTTCC 1617
1353 GGGGTGTTTACGAAATAAAGTATGGTTGGACGAGTCCGAAGACCTGACCGGTTTACTTCC 3812
1618 TGGAACTCCTAAATGGGATGTTTGGAGTCGGATATGATATGGCAGGACGATGACCGCC 1677
1353 TGGAACTCCTAAATGGGATGTTTGGCGTTGAGTGTATATGGAAGGAATGATGACCGCA 3872
1678 GATTTGGCTTCTTCTGCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGA 1737
1353 GATTTGGGTCTTCTGCTGCTCTAGAGTTTATCTCCAGAAATGAATTTCTCCAC 3932
1738 ACATATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1797
1353 ATATATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3992
1798 ACGGAAGTCTAGCTTGGCAACGACGAGTGGTATTCACCAATCCACAACTCTGAAATTTG 1857
1353 ATTCCCAATCCAGAAATGGACACTCGGGTTGATTTTACCAATCCACAACTCTGAAATTTG 4052
1858 GAGCGCATCATATTTGGCAAGCAATGAGATATGATATGAAGCAACAACTGCTCTTAATA 1917
1353 GAGCAATTTATTTGGTAAAGCAATGACATCTGCTGATTAAGCCCAACTGTTTCTCCTA 4112
1918 CATATTTCAAGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1977
1353 CATATTTCAAGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4172
1978 GAATTTCAATGGAATTTGATCCGATATATGGATCGGTACATGACAACTTTATCCCGG 2037
1353 GAATTTCAATGGAATTTGATCCAGATATCTGGATCCGTAAGTCAATTTATCCCGG 4232
2038 TCCACTACATTTGTGAAATGTTGTGAAGCAAGAGGCTGCTAAGAGGCACTGCGAGC 2097
1353 TCCCTTATATTTGTGAAATGTTGTGAAGCAAGAGGCTGCTAAGAGGCACTGCGAGC 4292
2098 AGAAGTTTGGGTACAGCAAAATGATGTTCCCGTGTAGGAATGCTCACTCGCTGACAG 2157
1353 AGAAGTTTGGGTACAGCAAAATGATGTTCCCGTGTAGGAATGCTCACTCGCTGACAG 4352

2158 CCCAAAGGGGATCCACCTGATCAAGCATCGGATTCACCGTACACTCGAAACGGAACGGAC 2217
4353 CCCGAAAGGAATCCACTCATCAAGCAGCAATTCACCGAACTCTCGAAAGCAACGGAC 4412
2218 AGGTGGTTTTGCTTGGTTCAAGCCCGGACTCTCGAAATCCAAAGCTGATTTTGTCAACCTGG 2277
4413 ATGTGGTTTTGCTTGGTTCAAGCTCCAGATCATCGAATACAAAGCGGATTTTTCGAGATTGG 4472
2278 CGAATAGCTTCCAGGGGTAACCATGGGCAAGTGGGCTTCTTTCGACCTACGACGAGC 2337
4473 CCGATGCTCTTCATGGTGTTCATCATGGTGAAGCTTGTCTAACCTATGATGAGC 4532
2338 CTCTCTCGCATCTGATATAGCTGGCTCTGACTTCAATCTTGGTCCCATCTATATTTGAGC 2397
4533 CTCTTCTCACTGATATAGCTGGCTCGACTTCATAATTTGTTCTTCAATCTTTCGAAAC 4592
2398 CTTGCGGCTTAACTAGCTCGTCCCATCGGATGGAACCAATCCCGGATTTTCGCAAGA 2457
4593 CTTGCGGCTTAACTAGCTTGTGCTATGGTATGATGATGATGATGATGATGATGATGATGATG 4652
2458 CTGAGGCTTCTTTCGACACTGCTTTCGATGTCGACATGACAAAGTGGTGGTGGTGGTGGTGG 2517
4653 CTGAGGACTTTCGACACTGCTTTCGATGTCGACATGACAAAGTGGTGGTGGTGGTGGTGG 4712
2518 GAGGCTTTCGACACTGCTTTCGATGTCGACATGACAAAGTGGTGGTGGTGGTGGTGGTGG 2577
4713 TTGCTTTCGACAAATGGTTCAGTTTCGACGAGCGGACGACGCAATGGCGTGGATATG 4772
2578 CGCTGAACAGGGCGATC 2594
4773 CCCTCAACAGAGCAATC 4789

RESULT 4

AAC86414
ID AAC86414 standard; cDNA; 3621 BP.

XX AAC86414;

XX 01-MAR-2001 (first entry)

XX Wheat starch synthase III coding sequence SEQ ID NO: 9.

XX Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
XX food product; adhesive; ss.

XX Triticum aestivum.

XX WO200066745-A1.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-AU000395.

XX 29-APR-1999; 99AU-0000052.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX (GOOD-) GOODMAN FIELDER LTD.

XX (LINA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX Morell M, Li Z, Rahman S, Appels R;

XX WPI; 2000-647602/62.

XX P-PSDB; AAB37570.

XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and WST-II,
XX useful in modifying plant starch content and/or composition.

XX Claim 1; Page 179-183; 211pp; English.

XX The present invention relates to novel protein and coding sequences from
XX wheat. The proteins are wheat starch synthases, designated SSII and
XX SSIII. These can be used in the modification of plant starch content or

CC composition, and to screen plants to identify mutations which affect
CC starch content and composition. The starch can then be used in food
CC products, such as flour, and in films, coatings, adhesives, building
CC materials and packaging materials

Sequence 3621 BP; 1060 A; 697 C; 904 G; 959 T; 0 U; 1 Other;

Query Match	67.1%;	Score 1744.2;	DB 3;	Length 3621;
Best Local Similarity	80.2%;	Pred. No. 0;		
Matches 2085;	Conservative	0;	Mismatches 509;	Indels 6;
				Gaps 3;

Qy	1	AGCTTGCCTGA	AAAATATTTTCGCTGGAAACAAGTTTGTTTACTTATTCACAGATGTATTGA	60
Db	455	AACTCGCTGAGA	AAAAATATTCGATGAGGAACAAGCTGTTTGTGTTTTTCCAGAGGTAGTGA	514
Qy	61	AAGCTGATTTCAA	CAATATGATCTCTATTTCATTCGTGATCTATCAGCTGTGGCCAAATGAGC	120
Db	515	AAGCTGATTTCA	GTATTGATCTTTTAAATCGTGACCTAAACAGCTTTGGCGNATGAC	574
Qy	121	CTGATGTACTTAT	CAAAAGGAGCATTCAAATGGTGGAAAGTGAGATTTTTTCACTGAAAAAT	180
Db	575	CCGATGTCGT	CATCAAAAGGAGCATTCAAATGGTGGAAATGAGGCTTTTCACTGAAAGAT	634
Qy	181	TGCACRAGAGCG	AGCTGGCAGGGGACCTGFTGGTCTGCAAACTATACATTCCTCPAAGCAGG	240
Db	635	TGCACAAGATG	ACCTTGGAGGGGTGTTGGTCTTGCAAACTGTACATACCCAAAGAGG	694
Qy	241	CATACAGAATCG	ACTTTGTGTGTTTTTAAACGGACACACAGCGTATATGAAAAATAAACAATA	300
Db	695	CCTACAGATTAG	ACTTTGTGTCTTCAAGGTGCGACGGTCTATGAGAACATATGGCAACA	754
Qy	301	ATGATTTCTGTG	ATACAAATGAAAGCCATATGAGATGAAAAATTTATTTGAGATTTCTTTGG	360
Db	755	ATGATTTCTGT	ATAGGAATGAGGCCATATGAATGAAGATCTGTTTGAAGATTTCTTTGG	814
Qy	361	CTGAAGAAAGCA	CGAGAACTTTCAGAACCTTGCAAATGAGGAGCTGAAAGGAGGAGAC	420
Db	815	TTAAGAAAAGCA	AAAGGAGCTTGAGAAACTTGGCCATGGAAAGAGCTGAAAGGAGGACAC	874
Qy	421	AAACTGATGAGC	AGCGGCGAATGAGGAAGAAAGGGCGCGCAGATAAAGCTGACAGGGTAC	480
Db	875	AGACTGAAGAAC	AGCGGGAAGGAAGCAAGGGCTGCAGATGAAGCTGCAGGGCAC	934
Qy	481	AAGCCAGGTTG	AGGTAGACGAGGAAGAATAAATTGTGCAATGTATTGGGTTTAGCCA	540
Db	935	AAGCGAAGGCG	AGATAGAGATCAGGAAGAAAAAATTTGCAAGTATGTTGAGTTTGGCCA	994
Qy	541	GAGCTCCTGTTG	ATAATTATGTGTACATTGAGCCCATCAGACCTGGACAAGAGGCTACTG	600
Db	995	GAACATGTTGT	ATAAATTTGTGTGCATAGAGGCTAGCAAGATACRAGAGGAGATACTA	1054
Qy	601	TCAGATTTGTTA	PAACATAAACTCAAGACCTCTAGTTTCACAGTACTGAGATATGGATGC	660
Db	1055	TCAGTTATATTA	TAAACAGAAACTCGAGGCCACTTGCGCATAGTACTGAGATTTGGATGC	1114
Qy	661	ATGCTGCTATA	AACTTGGATGATGGACTCTTTTGTCTGAAAGGCTTGTTCATCATC	720
Db	1115	ATGCTGGTTACA	AAATTTGGTCAGATGGACTCTCTATGTTTGAAGGCTTTGTCAAGTGCA	1174
Qy	721	ATGACAAAGAT	TTGTATTGTTGGTTTTGCAGATGTTGTGTCGCCCTGAAAGAACATATGTAT	780
Db	1175	ATGACAAAGCG	GCGATTGTTGTTATGCAAGATTTATTCACCTGGAANAAGCACTTGTGT	1234
Qy	781	TGGACTGGGTTTT	GCTGACGGCCCCACACGAGGATGCAAGGAATATGACAAACAATGAG	840
Db	1235	TGGACTGGGTTTT	GCTGATGGGCCAGCTGGGAATGCAAGGAACATATGACAAACAATGCTC	1294
Qy	841	GACATGATTTTC	ATGCTACCTTCCAAATACA---TGACTTGGGAGAGATTTGGATGG	897
Db	1295	GACAAGATTTCC	ATGCTATTCTTCGAAACAATATGTAACCGAGGAAGGCTTCTTGGCGC	1354
Qy	898	AAGAAGAACAA	AGGATCTATACAAGGCTTCAACAAGAGAGGAGGGAAGGAGGAGGCTA	957

QY 2035 CGGTCCACTACACTTGTGAGAAATGTTGTTGAAGGCAAGAGGGGTGCTTAAGAGGGCACTGC 2094
 Db 2495 CGGTCCCTTATATCTTGTGAGAAATGTTGTCGAAGGCAAGAGGGGTGCAAAAAGGGCCCTTGC 2554
 QY 2095 AGCAGAAAGTTGGTTTACAGCAATCGATGTCCTCCGTGTAAGAAATCGTCACTCGCTGA 2154
 Db 2555 AGCAGAAAGTTGGTTTACAGCAATCGATGTCCTCCGTGTAAGAAATCGTCACTCGCTGA 2614
 QY 2155 CAGCCAAAAGGGATCCACTCATCAAGCATGCGATTTCACCGTACACTCGAAGCGAAAG 2214
 Db 2615 CAGCAGAAAGGAAATCCACTCATCAAGCAGCGAATTCACCGAACCCTCGAGAGCAATG 2674
 QY 2215 GACAGGTGGTTTGTGTTGTTGTCAGGCGCGACTCTCGAATCCAGCTGATTTGTCAACC 2274
 Db 2675 GACAAGTGGTTTGTGTTGTTGTCAGCTCCAGTCCAGATCATCGAATACAAGGCGAATTTTGCAGAT 2734
 QY 2275 TGGCGAATACGCTCCAGGGCGTAACCATCGGCAAGTGAGGCTTTCCTTGACCTACGAGC 2334
 Db 2735 TGGCCGATGCTCTACGGGTGTTTACCATGGTAGGGTGAAGCTTGTCTAACCTACGATG 2794
 QY 2335 AGCCTCTCGCATCTGATATAGCTGGCTCTGACTTTCATTCTGGTCCCATCTATATTTG 2394
 Db 2795 AGCTCTTTCTCCTGATATAGCTGGCTCGACTTCATTATGTCCTTCAATCTTTG 2854
 QY 2395 AGCCTTGGCGCTTAACCTAGCTCGTGGCGATGCGGTATGGAACCATCCCGATTTGCCGA 2454
 Db 2855 AACCTGTGGCTTAACCAACTTGTGCGATGCGCTTATGGATCGATCCCTATATAGTTCCGA 2914
 QY 2455 AGACTGGAGGCTCTTCGACACTGCTTCGATGTTGGAATGCAAGCAAGAGCGCCGAG 2514
 Db 2915 AACCGGAGGACTTTACGACACTGCTTCGACGTAGACAATGATAGAACCGGCTCGT 2974
 QY 2515 ATCGAGGCTTGAGCCCAACCGGTTTAGCTTTGACGGAGCTGTATAGCAACGGTGTGACT 2574
 Db 2975 CTCTTGCTTGACCAATGAGTTTCAGTTTCGACGGGCGCAGCAATGCGGTGATT 3034
 QY 2575 ACGCGCTGAACAGGCGCATC 2594
 Db 3035 ATGCCCTCAACAGCAATC 3054
 RESULT 5
 ADA69827
 ID ADA69827 standard; DNA; 5760 BP.
 XX AC ADA69827;
 XX AC ADA69827;
 DT 20-NOV-2003 (first entry)
 XX DE Rice gene, SEQ ID 3150.
 XX DE Rice gene, SEQ ID 3150.
 XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.
 XX OS Oryza sativa.
 XX PN WO2003000898-A1.
 XX PD 03-JAN-2003.
 XX PF 22-JUN-2001; 2001WO-IB001105.
 XX PR 22-JUN-2001; 2001WO-IB001105.
 XX RA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.
 XX PT Identifying at least one gene involved in plant resistance or response to

pathogenic infection for conferring resistance or tolerance to a plant to
 bacterial, fungal or viral infection by determining or detecting plant
 gene expression.
 Claim 6; SEQ ID NO 3150; 899pp; English.
 The present invention relates to a method (M1) for identifying genes
 involved in plant resistance or response to pathogenic infection. M1
 comprises identifying a gene whose expression is significantly altered in
 the incompatible interaction of plant gene expression relative to
 the incompatible interaction of an uninfected plant, in a mutant plant that
 does not express a gene associated with response to pathogenic infection,
 or in a corresponding incompatible or compatible interaction. (M1) is
 useful for conferring resistance to resistance or tolerance to a plant to
 bacterial, fungal or viral infection. The present sequence was used to
 illustrate the invention.
 Sequence 5760 BP; 1762 A; 988 C; 1429 G; 1576 T; 0 U; 5 Other;
 Query Match 55.6%; Score 1703.8; DB 7; Length 5760;
 Best Local Similarity 79.2%; Pred. No. 0;
 Matches 2054; Conservative 0; Mismatches 497; Indels 42; Gaps 1;
 QY 1 AGCTTGTGTAAGAAATATTTTCCTGGGAAACAAGTTGTTTACTTATCCAGATGTAATGA 60
 Db 2648 AACTTGTGTAAGAAATATTTTCCTGGGAAACAAGTTGTTTACTTATCCAGATGTAATGA 2707
 QY 61 AAGCTGATTCACAAATGATCTCTATTTCAATCGTGAATCTATCAGCTGTGGCCAAATGAGC 120
 Db 2708 AGGCTAATTCGACAAATGATGATATTTGAATCGTAACCTATCGGCTTTGGCGAATGAGC 2767
 QY 121 CTGATGTACTTATCAAGAGGAGCATTCAAATGGGTGGAAAGTGGAGATTTTTCACCTGAAATAAT 180
 Db 2768 CTGATGTACTTATCAAGAGGAGCATTCAAATGGGTGGAAAGTGGAGATTTTTCACCTGAAATAAT 2827
 QY 181 TGCAAGAGGAGGAGCTGCGCAGGGGAGCTGGTGGTCTGCAAACTATACATTTCTTAAGCAGG 240
 Db 2828 TGCAAGAGGAGGAGCTGCGCAGGGGAGCTGGTGGTCTGCAAACTATACATTTCTTAAGCAGG 2887
 QY 241 CATACAGAAATGGACTTTGTTGTTTTCACGACACACGGTATATGAAATAATTAACATA 300
 Db 2888 CTTATAGATTAGACTTTGTTGTTTTCACGACACACGGTATATGAAATAATTAACATA 2947
 QY 301 ATGATTTTCGTGATACAAATAGAAAGCACCATGGATGAAATTTATTTGAGGATTTCTTTGG 360
 Db 2948 ATGATTTTCGTGATACAAATAGAAAGCACCATGGATGAAATTTATTTGAGGATTTCTTTGG 3007
 QY 361 CTGAAGAAAAGCAACGAGAACTTTGAGAACCTTGCAAATGAGGAAGCTGAAAGGAGGAGAC 420
 Db 3008 TTGAAGAAAAGCAACGAGAACTTTGAGAACCTTGCCACTGAAAGAGCTGAAAGGAGGAGGC 3067
 QY 421 AAAGTATGACGAGCGGGAATGAGGAAGAAAGGGCGGAGATAAGCTCAGAGGATAC 480
 Db 3068 ATGCTGAAGAGCAGCAGCGAATGGGAGAAACAAGGGCTGCAAGAACAGCTGCCAGGAGAC 3127
 QY 481 AAGCCAAAGTTGAGGTAGAGACGAGAAAGAAATAAATTTGCAATGATTTGAGGTTTAGCCA 540
 Db 3128 AGGCTAAGAGGAGATAGATTGAGGAAGAACAAATTTGCAAAATCTGTTGAGTTGAGCCA 3187
 QY 541 GAGCTCTGTTGTAATAATTTATGGTACATTTAGGCCCATCACGACTGGCAAGAGGCTACTG 600
 Db 3188 GAACACATGTTGATAATTTTGGGCACATAGAGCCCTAGCACATATAGACAGGGGACACTG 3247
 QY 601 TCAGATTGTATTAACATTAACCTCAGACCTCTAGTTTCACAGTACTGAGATATAGATGTC 660
 Db 3248 TCAGATTGTATTAACATTAACCTCAGACCTCTAGTTTCACAGTACTGAGATATAGATGTC 3307
 QY 661 ATGGTGGCTATAACAAATTTGGAATTTGATGACCTCTCTTTTGGTGAAGAGGCTTGTTCATCATC 720
 Db 3308 ATGGTGGTTCGAATAGTTGGACTGATGACCTCTCTATTTGTTGAAGAGCTTGTTCGATGTCG 3367
 QY 721 ATGACAAAGATTTGATTTGGTGGTTTCAGATGTTGCTGCTGCAAGAAACATATGATAT 780

Db 3368 ATGACGAAATGGTGATGTTGGTATGCTAATGTTCTATATACCTGAAAGAGCCCTTTGTAT 3427
 QY 781 TGGACTGGTTTTGCTGACGGCCACCAGGAGTGCAAGGAATATGACAAACAATGGAG 840
 Db 3428 TGGACTGGTTTTGCTGACGGGCCACTGGAATGCAAGGAATATGACAAACAATGGTC 3487
 QY 841 GACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGGAAGAGATTTGGATGGAG 900
 Db 3488 GACAAGATTTTCATGCTATTTCCAAATGCACTGACTTAACGAAGAAATTTGGGTGAAG 3547
 QY 901 AAGAACAAAGATCTATACAGGCTTCAACAGAGAGAGGGAAGGAGGAGGCTATT 960
 Db 3548 AGGAACCTGATCTATACAGGCTTCCACAGAGATCAGAGAACGGAGGAGGCTATT 3607
 QY 961 AAAGGAAGGCTGAGAGAATGCAAAATGAAAGCTGAGATGAAGGAAGAAAGACTATGAGAA 1020
 Db 3608 AATTAAGGTTGAGAAAGAGCAAAATGAAATCTGAGATGAAGGAAGAAAGACTATGAGAA 3667
 QY 1021 TGTTCCTGGTTCTCAGAAACACATGTTTACCCGAACCACTTGAATACATGCTGGAA 1080
 Db 3668 TGTTTCTACTTCTCAGAAACACATGTTTATCTGAAACCACTTGAATACATGCTGGAA 3727
 QY 1081 CTACTATTGATGCTTTATATCTCTCTATACAGTTCTACTGAAAGCCAGAGGTTT 1140
 Db 3728 CAACTGTGGATGTTCTATATATCTCTCTATACAGTTCTACTGAAAGCCAGAGGTTT 3787
 QY 1141 GGTTCGATGTTCTCTTAAATCGTTGATGTATCCAGGTGGGTGTTGCGACCTCAGAAGA 1200
 Db 3788 GGTTCGATGTTCTCTTAAACCGATGGATGCAATCCAGTGTGTTTACCAACCAAGAAGA 3847
 QY 1201 TGGTACAGCAGAAATGTTTCACTTAAAGCAACAGTTTACGTTCCACAGATGCTT 1260
 Db 3848 TGGTCAAAACAGAAATGTTTCACTTAAAGCAACAGTTTACGTTCCACAGATGCTT 3907
 QY 1261 ATATGATGACCTCTGTTTCTCGAGTCAAGAGAGTGGAAATTTATGATAACAGAAATG 1320
 Db 3908 ATATGATGACCTCTGTTTCTCGAGTCAAGAGAGTGGAAATTTATGATAACAGAAATG 3967
 QY 1321 GGTGATGATCATATCTCTGTTTCTGTTTGGTCAATTTGCAAGGAACCACTATGCAATG 1380
 Db 3968 GACAGACTATCATATCTCTGTTTCTGTTTCCAATGCAAGGAGCCTCCCATTCATATTG 4027
 QY 1381 TCCACATGCTGTTGAGATGGCAACCAATCGCAAGGTTGAGGTTCTGTTGATGTTGCA 1440
 Db 4028 TCCATATAGCGTTGAGATGGCAACCAATCGCAAGGTTGAGGTTCTGTTGATGTTGCA 4087
 QY 1441 CTAGTCTTTCAGTCTGTTGCAAGATTTAGGACACAATGTTGAGGTTTATCTTCCAAAGT 1500
 Db 4088 CAAGTCTTTCAGTCTGCAATTCAGAGTTAGGCCATCATGTTGAGTTTATCTCCGAAAT 4147
 QY 1501 ACGGTTGCTTGAATCTAAGCAATGTTCAAGAAATCTCAAAATCCATCAGAGTTTCTTGG 1560
 Db 4148 ATAAATTTTATGAATCAAGCAATGTTGAAGATTTGCAATGTTGCAATGTTGCAATGTTG 4207
 QY 1561 GTGGTTCTGAATTAATGTTGGCTGAGTCTGAGGCTTCTGTTTACTTCTCTG 1620
 Db 4208 GTGGTACAGAAATTAAGTGTGGTGGATGTTGAGGCTTCTGTTTACTTCTTGG 4267
 QY 1621 AACCTCAAAATGGGATGTTTGGAGTGGATATGATATGCGAGGACGATGACCGCGAT 1680
 Db 4268 AACCTCAAAATGGGATGTTTGGGTTGGATGTTGAGGACGATGTTGCGAGAT 4327
 QY 1681 TTGGCTTCTTCTGCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAAACA 1740
 Db 4328 TTGGCTTCTTCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAAACA 4387
 QY 1741 TAATACATTCCTGATGTTGCTGAGTCTCTGTTGCTGCTGCTACACAAGGAATCTACG 1800
 Db 4388 TAATACATTCCTGATGTTGCTGAGTCTCTGTTGCTGCTGCTATACAAGGAACACTATG 4447
 QY 1801 CGAAGTCTAGCTTGGCAAAACGACGGTGGTATTTCAGCATCCCAATCTTGAATTTGGAG 1860
 Db 4448 CAGATCCAGGTTGGCAAAACGACGGTGGTATTTCAGCATCCCAATCTTGAATTTGGAG 4507

QY 1861 CGCATCATATTTGGCAAGCAATGAGATATTTGTATGAAGCAACAACCTGCTCTAATCAT 1920
 Db 4508 CACATTTTATTTGAAAGCAATGACATCTGCGCAAAAGCCAACTGTTTCTCACAGT 4567
 QY 1921 ATTCAAAGGAAGTGTCAAGTCAATGTCCTGATGTTTCTGGAATTTCTTGGAAATTTCTATGGCA 1980
 Db 4568 ATTCAAAGGAAGTGTCAAGTCAATGTCCTGATGTTTCTGGAATTTCTTGGAAATTTCTATGGAA 4627
 QY 1981 TTCTCAATGGAATTTGATCCCGATATATGGAATTCGTACAAATGACAACTTTATCCGGTCC 2040
 Db 4628 TTCTCAATGGAATTTGATCCCGATATCTGGATTCATATCTGATAAATCTTATCCCGATGC 4687
 QY 2041 ACTACACTTTGGAATTTGTTTGAAGCAAGGCTGTTAAGAGGCACTGACAGCAGA 2100
 Db 4688 ATTATATCTTCTGAAATTTGTTTGAAGCAAGATGTTGCAAAAGAGCANTTGCAGCAGA 4747
 QY 2101 AGTTTGGGTTTACAGCAATCGATGTTCCCGTCTGTAAGAAATCGTCACTGCTGACAGCCC 2160
 Db 4748 GTTTGGACTGACAGACTGATGTTCCCAATTTGTTGGAATCATCACTGTTGACAGCCC 4807
 QY 2161 AAAAGGGGATCCACTGATCAAGCATGCGATACCGTACACTCGAACGGAACGACGAGS 2220
 Db 4808 AGAAGGGTATCCACTCAATTAACATGCACTTCACTCGGACACTTTGAACGCAATGGACAGG 4867
 QY 2221 TGGTTTGTGTTTTCAGGCGGACTCTCGAATCCAAAGCTGATTTTGTCAACCTGGGGA 2280
 Db 4868 TGGTTTGTGTTTTCAGGCGGACTCTCGAATCCAAAGCTGATTTTGTCAACCTGGGGA 4927
 QY 2281 ATACGCTCCAGGGCTAAACCATGGGCAAGTGAAGGCTTTTCTTGTACCTACGACGAGCCTC 2340
 Db 4928 ATAGTCTTTCATGGTGAACCAATG- 4952
 QY 2341 TCTGCACTGATATGATGATGCTGCTCTGATCTTCACTTCTGTTCCCATCTATATTTGAGCCTT 2400
 Db 4953 -----CAGGATATGCTGCTCTGATCTTCACTTCTGTTCCCATCTTGAACCTT 5005
 QY 2401 GGGGCTTAACCTCAGCTCGCTCGCATGCGGATGGAACCATCCGATTTGTCGCAAGACTG 2460
 Db 5006 GGGGTTGACTCAACTGTTTGCATGCGCTATGGAATCCATCCCTATTTGTCGGAACCG 5065
 QY 2461 GAGGGCTCTTCCACACTGTTTTCGATGTTGGAACAATGACAAAGGAACGAGCCGAGATCGAG 2520
 Db 5066 GAGGACTTTACGACACTGTTTTCGACGTAGACCAATGACAAAGACCGGCTCGAGTTCTAG 5125
 QY 2521 GCTTGAAGCCCAACGGGTTTACCTTTGACGAGCTGATAGCAACGCTGTTGACTACGCGC 2580
 Db 5126 GCTTGAACCAAAATGGGTTTCAGCTTTGATGAGCTGACTGTAATGTTGTTGATACGCCC 5185
 QY 2581 TGAACAGGCGCAT 2593
 Db 5186 TGAACAGGCAAT 5198
 RESULT 6
 ADA70734
 ID ADA70734 standard; DNA; 3645 BP.
 XX ADA70734;
 AC AC
 XX 20-NOV-2003 (first entry)
 DT DT
 XX
 DE Rice gene, SEQ ID 4057.
 XX Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.
 KW
 XX Oryza sativa.
 OS
 XX WO200300898-A1.
 FN
 XX 03-JAN-2003.
 PD
 XX

QY	1681	TTGGGCTCTTCTGTCGTCTCTAGAGTTTCTCCTCAAAGTGGATCTTCTCCGAACA	1740
Db	2606	TTGGGCTCTTCTGCGCAATCTGCTTAGAGTTTCTCGGCAAAATGGATCTTCTCTGATA	2665
QY	1741	TAATACATTTGCCATGATTGGTCAAGTGTCTCTGTTGGCTTGGCTACACAAGGAAATACG	1800
Db	2666	TTATACATTTGTATGATTGGTCAAGTGTCTCAAGTTGCTTGGCTATTCAAGGAAACAATATG	2725
QY	1801	CGAAGTCTAGTTGGCAAAACGACGGGTGGATTACCAATCCACAATCTTGAATTTGGAG	1860
Db	2726	CTCAAAATGSACTGTCAAATGGGCGGGTTGTATTTACCATCCACAACCTTGAATTTGGTG	2785
QY	1861	CGCATCATATTGCCAAGCAATGAGATATTGTGATAAAGCAACAACCTGTCTCTAATACAT	1920
Db	2786	CACATCACATCGGCAAGCAATGGCAAGTTGTGATAGGCTACCACTGTTTCATATAGT	2845
QY	1921	ATTCAAAGGAAGTGTCAAGTTCATGGTCCCATAGTTCTCCTCATTTGGGAAATCTTATGGCA	1980
Db	2846	ATTCAAGGGAAGTGTCAAGACATGGTGTCTATTGSCCCTCACTTTCCAAATTCACGGTA	2905
QY	1981	TTCTCAATGGAATTGATCCGGATATATGGGATCCGTGTAATGACAACCTTATCCCGGTCC	2040
Db	2906	TTCTGTAACGAATTGATCCAGATATTGGGATCCATACAGTGAACAATTTATCCCGGTCC	2965
QY	2041	ACTACACTTGTGAGATGTGTTTGAAGGCAAGAGGCTGCTAAGAGGCACTTCGACGAGA	2100
Db	2966	ACTATACCTCTGAGAATGTGTTGAGGGCAAGAGTGTCTGCCAATAAGAGCAATTGCACAGA	3025
QY	2101	AGTTTGGGTTTACAGCAATCGATGTCCCCGTCTAGGAAATCGTCACTCGCTCGACAGCCC	2160
Db	3026	GGCTTGGACTACAGCAACTGATACCCCTGTTGTGGAAATATCACTGCTGACAGTCC	3085
QY	2161	AAAAGGGGATCCACTTGATCAAGATTCGGATTCACCGTTACCTCGAAACGGACGGACGG	2220
Db	3086	AGAAGGGAATTCACCTTATCAAAACATGCAATTTATCGAACTCTTGAACGCAATGGCGAGG	3145
QY	2221	TGTTTTGCTTGGTTTACGCGCGGACTCTCGAATCCAAGCTGATTTTGTCAACCTCGGCA	2280
Db	3146	TGGTTTTACTAGGCTCAGCTCCAGATCATCGCATACAAGGTGACTTTTACCACTTAGCTA	3205
QY	2281	ATACGCTCCACGGGTAAACCATCGGCAAGTGTAGGCTTTCCTTGACCTACGACGAGCCTC	2340
Db	3206	GTAACCTGCATGGCGATACAATGGTGTGTAAAGCTTTGTTTAACTATGATGAGCCAC	3265
QY	2341	TCTCGCATCTGATATACGCTGGCTCTGACTTTCATTTCTGGTCCCATCTATATTTGAGCCTT	2400
Db	3266	TATCTCATTTGATTTATGCTGGTCCGACTTCATCTTGTTCCTTCCATGTTTGAACCTT	3325
QY	2401	CGGGCTTAACCTCAGCTCGTCCCATGGGTATGAAACCATCCGATGTCCGCAAGACTG	2460
Db	3326	GTGGTTTTAACCCAGCTTACTGCTATGGTTATGGATCTATCCCAATAGTTTCGGAAAACG	3385
QY	2461	GAGGGCTCTTCGACACTGTCTTTTCGATGTGGCAATGACAAGGAACGAGCCGAGATCGAG	2520
Db	3386	GAGGCCTTTATGACACCGTTTGTGACGTGCAAGTATGATAGGATCGAGCTCGAGAACAG	3445
QY	2521	GCCTTGAGCCCAACGGGTTTAGCTTTTGAACGAGCTGTATAGCAACGGTGTGATACGGCC	2580
Db	3446	GTCTTTGAGCCAAACGGTTTCAGTTTTCGAAGGAGCTGACAGCAACGGTGTGATTACGCC	3505
QY	2581	TGAAACAGGCGGATCTC	2596
Db	3506	TTGACAGAGCGATCAC	3521

RESULT 7
ADC07865
ID ADC07865 standard; DNA; 3032 BP.
XX
AC ADC07865;
XX
DT 18-DEC-2003 (first entry)

XX	Rice DNA sequence Seq ID131 related to grain filling.	
XX		
XX	plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;	
XX	carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;	
KW	tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;	
KW	wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;	
KW	gene; ds; plant.	
XX		
XX	Oryza sativa.	
OS		
XX	WO2003000905-A2.	
PN		
XX	03-JAN-2003.	
PD		
XX	21-JUN-2002; 2002WO-IB002450.	
FF		
XX	22-JUN-2001; 2001US-0300112P.	
XX	26-SEP-2001; 2001US-0325277P.	
PR		
PR	20-DEC-2001; 2001US-0342327P.	
XX		
XX	(SYGN) SYNGENTA PARTICIPATIONS AG.	
PA		
XX		
XX	Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;	
PI	Glazebrook J, Katagiri F, Krepis J, Provart N, Ricke D;	
PI		
PI	WPI; 2003-229341/22.	
DR	P-FSDB; ADC07866.	
DR		
XX	New plant genes encoding polypeptides having an activity involved in or	
PT	associated with the synthesis, metabolism or degradation of carbohydrates	
PT	in the plant grain useful in generating plants having improved	
PT	nutritional properties.	
XX		
XX	Claim 2; SEQ ID NO 131; 130pp; English.	
PS		
XX	This invention, in the area of plant biotechnology, relates to novel	
CC	polynucleotides comprising a nucleotide sequence encoding a protein which	
CC	is involved in or associated with the synthesis, metabolism or	
CC	degradation of carbohydrates in the plant grain and the expression of	
CC	which is up-regulated during grain filling. The plant is selected from	
CC	corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,	
CC	sugarbeet, wheat, and rice. The invention may be useful for the	
CC	improvement of protein, oil, starch, fibre and moisture content of the	
CC	cereal grains. In addition, carbohydrate levels may be modified to a more	
CC	desirable level using the present invention. The present sequence is a	
CC	DNA sequence encoding a rice protein of the invention. Note: The sequence	
CC	data for this patent did not form part of the printed specification, but	
CC	was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/publishedpct_sequences.	
XX		
XX	Sequence 3032 BP: 873 A: 597 C: 735 G: 827 T: 0 U: 0 Other;	
SC		

	Query Match	60.9%;	Score 1581.4;	DB 9;	Length 3032;
	Best Local Similarity	77.5%;	Pred. No. 0;		
	Matches 2048;	Conservative	0;	Mismatches 491;	Indels 102; Gaps 7;
Qy	1	AGCTTGCTGAAAAAATTTATTCGCTGGCAACAAGTTGTTTACTTATCCAGATGATATGA	60		
Db	323	AATTTGCTGACCAGATTGTTTCATGGGTAAACAGCTTTTCGTTTTCCAGAGGCAGTGA	382		
Qy	61	AAGCTGATTCAACAATTGATCTCTATTTCATTCGTGATCTATCAGCTGTGGCCAAATGAGC	120		
Db	383	AGGCTTAATCGACAATTGATGTATATTGTAATCGTAACCTATCGGCTTTGGCGAATGAGC	442		
Qy	121	CTGATGTACTTATCAAGAGGAGCATTCATGGGTGGAAAGTGAGATTTTTCACTCAAAAAT	180		
Db	443	CTGATGTCCACATCAAGAGGAGCATTCATAGTTGAGATGAGGGCCCTTCAACGAAAGAC	502		
Qy	181	TGCAACAAGAGCGAGCTGGCAGGGGACTGGTGGTCTGCAAACTATACATTCCTTAAGCAGG	240		
Db	503	TGCAACAAGAGGATTCAGTGGGATTTGGTGGTCTTGCAAACTGCATACCCAGGAAG	562		

Db 2666 TGCTGGCTCTGACTTCATCCCTTGTTCCATCCATCTTTGAACTTGGCTTTGACTCAACT 2725

Qy 2417 CGTCGCCATGCGGTATGAACATCCCGATTGTGCGCAAGACTGGAGGG-CTCTTGGACA 2475

Db 2726 TGTGGCCATGCGTATGATCCATCCCTATTGTTGGGAAACCGGAGGACTTTACGACA 2785

Qy 2476 CTGCTTTGATGTGACATGACAGGAAACGAGCCGAGATCGAGGCTTGAGCCCAACG 2535

Db 2786 CTGTTTTCGACGTAGACCATGACAAAGACCGGCTCGAGTCTTAGGCTTGAACCAATG 2845

Qy 2536 GGTTTAGCTTTGACGAGCTGATAGCAACGCGTGTGACTTACGCGTGAACAGGCGGATCT 2595

Db 2846 GGTTCAGCTTTGATGAGCTGACTGTATGTTGTTGATGATACGCCCTGAACAGAGCAAT 2905

Qy 2596 C 2596

Db 2906 C 2906

RESULT 8

AAF61270

ID AAF61270 standard; cDNA; 4121 BP.

XX

AC AAF61270;

XX

DT 25-MAY-2001 (first entry)

XX

DE Maize starch synthase protein encoding cDNA.

XX

XX Starch synthesis; starch synthase; maize; transgenic plant; nutrition;

KW modified starch; starch storage; ss.

XX

OS Zea mays.

XX

EH Key

FT 442..3954

FT /*tag= a

FT /product= "starch synthesis associated protein"

XX

PN DE19937348-A1.

XX

XX 22-FEB-2001.

XX

PF 11-AUG-1999; 99DE-01037348.

XX

PR 11-AUG-1999; 99DE-01037348.

XX

XX (AVET) AVENTIS CROPS SCIENCE GMBH.

PA Froberg C;

PI

XX WPI; 2001-236028/25.

DR P-PSDB; AAB70781.

XX

XX New nucleic acid encoding a starch synthase isoform from maize, used to

PT produce recombinant plants that produce starch with modified properties.

XX

PS Claim 1b; Page 19-26; 32pp; German.

XX

XX This invention describes a novel nucleic acid (I) encoding a protein

CC (II) or its active fragments, with starch synthase (SS) activity

CC encoding a 1170 residue amino acid sequence (S2) comprising a 4121 base

CC pair sequence (S1), both fully defined in the specification, or its

CC complement, or containing the coding region of the cDNA insert in plasmid

CC IR65/87 (DSM 12970) or its complement. The invention also describes (1)

CC vector containing (1); (2) host cell, or transgenic plant cell, that

CC contains (1) or the vector of (1), or is derived from such a cell; (3)

CC (11), or its active fragments, encoded by (1); (4) production of (11), or

CC its active fragments, by culturing cells of (2); (5) plant containing

CC transgenic cells of (2), and their replicative material; (6) production

CC of the plants of (5); (7) starch produced by the plant cells of (2) or

CC the plants of (5), or their replicative material; and (8) production of

CC modified starch by extraction from the plant cells of (2) or the plants

CC of (5), or their starch-storing parts. (I) is used to prepare transgenic

CC plants (specifically maize) that have reduced or increased ss activity,

CC resulting in formation of starch with different chemical and/or physical,

CC and functional, properties, particularly altered viscosity and gel-

CC forming properties. Fragments of (I) can also be used as probes to

CC isolate related sequences from other organisms, also as antisense

CC inhibitors of ss activity. The starch produced by the transgenic plants

CC is useful for all usual nutritional and non-nutritional applications.

CC Modified starch may be better suited to particular applications

XX

SQ Sequence 4121 BP; 1180 A; 829 C; 1119 G; 993 T; 0 U; 0 Other;

Query Match 57.8%; Score 1500.4; DB 5; Length 4121;

Best Local Similarity 74.4%; Pred. No. 0;

Matches 1934; Conservative 0; Mismatches 601; Indels 63; Gaps 1;

Qy 1 AGCTTGCTGAAAAAATATTTCGCTGGGAAACAAGTGTCTTACCTTATCCAGATGATTGA 60

Db 1298 AGCTTGCTGATGAGAAATATTTCGACTGGGAAACAATGTTTGTTCCTCGAAGTAGTGA 1357

Qy 61 AAGCTGATTCACACATTCATCTCTATTTCATCTGATCTATCAGCTGTGGCAATGAGC 120

Db 1358 AGGCTGATTCGATGATGATCTTACTTAAACCGCAGCATGTCGCGCTTAGTAGTGTAGT 1417

Qy 121 CTGATGTACTTTATCAAGGAGCAATCAATGGGTGGAAGTGGAGATTTTTCACCTGAAAAAT 180

Db 1418 CCGAGCTTTTGTAAAGGAGCAATCAATGGTGGAGATGGAACCGTTTTCACCTGAAAAA 1477

Qy 181 TGCACAAGAGCAGCTGGCAGGGGACTGGTGTGTGCTGCAAACTATACATCTCTCAAGCAG 240

Db 1478 TGCATAGAAGCGAATTAAGAGGGGATTTGGTGTGTGCTGCAAGCTCTACATTCGCAAGCAG 1537

Qy 241 CATACAGATGACATTTGTGTTTTTAAACGGACACACGCTATATGAAATAATAACAATA 300

Db 1538 CATACAGACTGACTTTGTATTCTTTAAACGGTGACACTGTCTTATGAAATTAACAATCA 1597

Qy 301 ATGATTTTCGTGATACAAATPAGAAAGCACCATGGATGAAATAATTTATTGAGGATTTCTTGG 360

Db 1598 ACGATTTTTCCTGGAAATAGAAAGTGACATAGATGAACACTCATTTGAGGACTTCTTGG 1657

Qy 361 CTGAAGAAAGCAACGAGAACTTGAGAACTTGCACATGAGGAGCTGAAAGGAGGAGAC 420

Db 1658 TTGAAGAAAGCGAAAGAAAGTCTGAGAGGCTTGCCTGCAAGAAAGCTGAAAGAAAGAC 1717

Qy 421 AAACCTGATCAGCAGCGCGCAATGGAGAAAGAGGCGCCGACAGATAAAGCTGACAGGCTAC 480

Db 1718 AAGCTGAGAGCGGACACAGAGAGAGAGAGAGAGGCGCGGATGGAGCTGACAGGAC 1777

Qy 481 AAGCCAAAGTTGAGGTAG 540

Db 1778 AAGCAAGGCTCGAGGTCGAGATGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1837

Qy 541 GAGCTCTGTTGATTAATTTATGATATGATGAGGCGCCATCAGCTGACAGAGAGAGAGAG 600

Db 1838 GCAGATATGCTGAGAACTTATGATACATAGAACTTAACACCTACAGAGAGAGAGAGAG 1897

Qy 601 TCAGATTGTATTATAACATAAACTCAAGACCTTAGTTCACAGTACTGAGATATGAGATGC 660

Db 1898 TTGATTTGACTATAATAGAGCTCGAGTCACTATGATACATGATGATGATGATGATGAT 1957

Qy 661 ATGGTGGCTATAACAATGGATGATGAGTCTCTTTTGTCTGAAAGGCTTTGTCATCATC 720

Db 1958 ATGGAGTTTATAACAACACTGGATGATGAGTCTCTCAATAGCTGAAAGACTTGTCAAAATCTC 2017

Qy 721 ATGACAAAAGATTTGATGTTGGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

Db 2018 ATGAAAAGGAGGCGGATTTGGTGTATGTAGAGTTTACATTTACCTGAAAGGCGCATTTGGTGT 2077

Qy 781 TGGACTGGGTTTTTGTCTGACGGGCGCCACAGGGAGTGCAGAGAAATATGACAAATGGAG 840

Db 2078 TGGATTGGGTTTTTGTCTGATGGACCCACCTGGGAAATGCAAGGAATTTATGATAACATGGAA 2137

Qy 841 GACATGATTTTTCATGCTACTCCCTTTCCAAATAACATGACTGAGGAGAGATTTTGGATGGAAG 900

Db 2138 GGCAGGATTTTCATGCCATCTTCTTAATACATATCGATGATATCTTTGGTGGAG 2197
QY 901 AAGAACAAAGGATCTATACAGGCTTCAACAAAGAGAGAGGAGGAGGCTATTA 960
Db 2198 AAGAACATAGGATCTTACAGGCTTCAACAAAGAGAGAGAGGAGGAGTCCGAAA 2257
QY 961 AAGGAAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAGGAAAGCTATGAGAA 1020
Db 2258 GAATAAAGGCTGAGAGATCTGCAAAATGAAAGCTGAGATGAAGGAAAGCTATGAGAG 2317
QY 1021 TGTCTCTGTTCTCAGAAACACATGTTTACACGACCACTTGAATACATACATGCGAA 1080
Db 2318 CGTTCTGCTCTCAAAACATATGTGTATATCTGAGCCACTGAGTACGTCAGGAA 2377
QY 1081 CTACTATTGATGTCTTATATCTTCAATACAGTTTCTAACTGGAAAGCCAGAGTTT 1140
Db 2378 CCACTGTGAGCTTCTTATATCTTCTAACAACAGTCTGAATGGAAAGTCAGAGGTTT 2437
QY 1141 GGTTCGATGTCCTTAAATCGTTGGATGATCCAGGTGGGTGTGCGACCTCAGAGA 1200
Db 2438 GGTTCAGAGGTCCTTTAAACCGTTGGAATCTCAACAGTGGTCCCTTACCAACACAGAGA 2497
QY 1201 TGGTCAAGCAGAAATGGTTCAACACTTAAAGCAACAGTTTACGTTCCACGAGATGCT 1260
Db 2498 TGGTAAAGGCTGAGATATGTTTCAACACTTACGACACAGTCTGAGTCTCCCTGGATGAT 2557
QY 1261 ATATGATGAGCTCGTTTCTCGAGTCAAGAAAGGTGGAATTTATGATACAGAAATG 1320
Db 2558 ATATGATGAGCTTCTTCTGAGTGGAGAAAGGTGGAAGATATGACATATGGAACG 2617
QY 1321 GGTGATCATCATATCTGTTTGGTCAATTCGAAAGCAACCACTATGACATG 1380
Db 2618 GGTGATGATCATATCTGTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 2677
QY 1381 TCCATATGCTGTTGAGATGGCAACCAATCGCAAGGTTGAGGCTCTGGTATGTTGCA 1440
Db 2678 TACATATGAGTGAATGGTCTCTACGCAAGGTTGGAGGCTTGGTATGTTGTA 2737
QY 1441 CTAGTCTTTCAGTGTGCAAGATTTAGGACACATGAGGAGTATCTTCCAAAGT 1500
Db 2738 CAAGCCTTTCAGAGCTGTTCAGGATTTAGGCAATAAAGTTGAGGTTATCTTCCGAAAGT 2797
QY 1501 AGGTTGCTGATCTAAGCAATGTCAGAAATCTACAAATCCATCAGAGTTTCTTGGG 1560
Db 2798 ATGATGTTTAAATCTTAACAGTGTGAAGATTTAGGCAATAAAGTTGAGGTTATCTTCCGAAAGT 2857
QY 1561 GTGGTTCTGAAATAAATGTGCGGTGGACTAGTCGAAGGCTTTGTGTTTACTTCTCGG 1620
Db 2858 GTGGCACAGGTTAAAGATATGTTTGGAAAGGTTGAAGATCTGCCAGTTTACTTCTTGG 2917
QY 1621 AACCTCAAAATGGAGTGTGGAGTCGATATGATATGCGAGGACGATACCCCGAT 1680
Db 2918 AACCAAAATGGCATGTTTGGGTTGGATGTGTATGCGAAGATGATGAGAGTAGAT 2977
QY 1681 TTGGCTTCTCTGCTCTGCTCTAGAGTTCTCTCCAAAGTGGATCTTCTCCGAAAC 1740
Db 2978 TTGGCTTCTCTGCTCTGCTCTGAGTTCTCTCCAAAGATCTTCTCCGATGAT 3037
QY 1741 TAATACATTTGCCATGATTTGGTCAAGTCTCTGTTGCTGGCTGACACAGGAAATACG 1800
Db 3038 TCATACATTTGTCATGACTGGTCAAGTCTCCGCTTGGCTATACAAAGGACAGTATG 3097
QY 1801 CGAGTCTAGCTTGGCAACGACCGGTTGATTTACCATCCACATCTTGAATTTGGAG 1860
Db 3098 CTCTTAATGGGCTGGAAATGGTTCGAGTTGATTTTACCATCCACATCTGAGTTGGAG 3157
QY 1861 CGCATCATATTTGCAAGCAATCAGATATTTGTATAAAGCAACAACTGCTCTTAACAT 1920
Db 3158 CGCATCATATTTGCAAGCAATTTGCAATTTGCAAGGCTCACTGCTCTGATACAT 3217
QY 1921 ATTCAAGGAAGTCTCAGGTCATGTTGCCATAGTTCTCTCATCTTGGAAATCTATGGCA 1980

Db 3218 ATTCAAGGAAGTGGCTGGACATGAGCTATTGCACTACTACTATAAAATTCATGGAA 3277
QY 1981 TTCTCAATGAATTTGATCCGATATATGGGATCGTACATGACAACTTTATCCCGTCC 2040
Db 3278 TTGAAATGGAATTTGATCTGACATTTGGGATCCATATATGACAGATTTATCCGGTTC 3337
QY 2041 ACTACACTCTGTGAGATGTGTTGAAGGCAAGAGGCTGTGAAGAGGCACTTGACAGAGA 2100
Db 3338 ATTATACATCAGAGATGTTCTTGAAGGCAAGGCTGTGCAAAAAGGCAATTGACAGAGA 3397
QY 2101 AGTTTGGTTTACAGCAATCGATGTCCTCCCTGTGTAAGAACTGCTGCTGACAGCCC 2160
Db 3398 TGCTTGGATTACAGCAACTGATAGCCCTGTGTTGGAATCATCATCTGCTAAACAGTGC 3457
QY 2161 AAAAGGGATCCACCTGATCAAGCATCGGATTCACCGTACACTCGAACGGAAACGACAGG 2220
Db 3458 AGAAGGGAATCCACCTTATCAACATGCAATGCAATGCACTCTTGAACGCAATGGGACG 3517
QY 2221 TGGTTTGTGTTTACGCGCGGACTCTCGAATCCAAAGCTGATTTTGTCAACCTGGCGA 2280
Db 3518 TGGTTTACTGGGTTCTGCAACAGATCATCGCATACAAGGTGACTTTACAAATTTAGCCA 3577
QY 2281 ATACGCTCCAGCGGCTAAACCATGGGCAAGTGAAGCTTCTTGAACCTACGAGGCTC 2340
Db 3578 GTAAGCTGCATGTTGAATACCATGGCGGCTGAAGCTATGTTTAACTTATGACGAGCCAC 3637
QY 2341 TCTCGCATCTGATATACGCTGGCTCTGACTTCAATCTGCTGCCATCTATATTGAGCCTT 2400
Db 3638 TGTCACTTT----- 3647
QY 2401 CGGCGCTAACTCAGCTCGTCCGATGGGTATGGAACCATCCGATTCGCGCAAGCTG 2460
Db 3648 -----GCTTATGCTATGCTACGATCCATCCGATTTGTCGAAAACTG 3694
QY 2461 GAGGCTCTTGCACACTGCTTCTGATGAGCAATGACAAAGACGAGCCGAGATCGAG 2520
Db 3695 GAGGCTCTTGCACACCGCTTGTGACGTCGACGATGATGAAGATCGGCTCAAGCACAG 3754
QY 2521 GCCTTGAGCCCAACGGGTTTGTAGCTTTGACGAGCTGTAGCAACCGTGTGACTACGGCC 2580
Db 3755 GCCTGACGCAATGGATTCAGTTTCGAGGAGCTGTAGCAGTGTGTAGATTATGCTC 3814
QY 2581 TGAACAGGCGGATCTAG 2598
Db 3815 TCGACAGAGCTATAACCG 3832

RESULT 9

AAT68646
ID AAT68646 standard; cDNA; 4127 BP.

XX AAT68646;

XX AC

XX 17-OCT-2003 (revised)

DT 16-AUG-1997 (first entry)

XX

XX Potato soluble starch synthase cDNA.

XX

KW Starch synthase; transgenic plant; potato; rice; Oryza sativa; tomato;

KW Lycopersicon esculentum; wheat; Triticum aestivum; cassava;

KW Manihot esculenta; sweet potato; Ipomoea batatas; barley;

KW Hordeum vulgare; oat; Avena; maize; Zea mays; ds.

XX

OS Solanum tuberosum; cv. Desiree.

XX

FH Key Location/Qualifiers

CDS 143..3835

FT /*tag= a

FT sig_peptide 143..322

FT /*tag= b

FT mat_peptide 323..3832

FT /*tag= c

XX

PN EP779363-A2.
 XX 18-JUN-1997.
 XX 11-DEC-1996; 96EP-00309004.
 XX 12-DEC-1995; 95GB-00025353.
 XX (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX Smith RM, Marshall J, Edwards EA, Martin CR;
 PI WPI; 1997-312737/29.
 XX P-PSDB; AAW17785.
 DR Soluble starch synthase - used to produce altered starch from
 DR commercially important plants, e.g. potato, rice, wheat, and maize.
 PT Claim 16; Page 18-24; 39pp; English.
 XX
 XX A composite cDNA sequence (AA178646) codes for a 100-140 kDa potato
 CC soluble starch synthase (AAW17785). The sequence was deduced from 2
 CC overlapping cDNA clones obtained from a tuber cDNA library by
 CC immunoscreening with antiserum raised against purified starch synthase.
 CC Starch synthase nucleic acids can be linked to a plant promoter, in sense
 CC or antisense direction, and used to alter starch characteristics in
 CC transgenic plants, esp. potato, tomato, rice, wheat, pearl cassava, sweet
 CC potato, barley, oat or maize. A novel altered starch, extracted from such
 CC transgenic plants, has a viscosity onset temperature that is reduced by
 CC at least 5 degC compared to starch from non-transformed plants. (Updated
 CC on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 4127 BP; 1282 A; 709 C; 977 G; 1159 T; 0 U; 0 Other;
 Query Match 46.4%; Score 1204.8; DB 2; Length 4127;
 Best Local Similarity 66.7%; Pred. No. 0;
 Matches 1735; Conservative 0; Mismatches 862; Indels 3; Gaps 1;
 2 GCTTGTGAAAAAATTTTCGCTGGGAAACAAGTTGTTTACTATTCAGATGATGATGAA 61
 1111 GCTTGTGAAAAAATTTTCGCTGGGAAACAAGTTGTTTACTATTCAGATGATGATGAA 1170
 62 AGCTGATTCACAAATGATCTCTATTCTTCAATCGTGTATCTATCAGCTGTCGCAATGAGCC 121
 1171 ACCTGATGAAGATGTCAGATATTTCTTAACAGAGTCTTTCACATTTGAAGATGATGTC 1230
 122 TGATGTACTTATCAAGAGGAGCATTCATGCTGGTGGAGTGGAGATTTTCTCACTGAAAAAT 181
 1231 TGATGTCTTATGAGAGCTTTTAAATGAGTGGCGCTATAGGTCTTTTACTACAGGCT 1290
 182 GCACAGAGGAGCTGCGAGGAGCTGCTGGTGTGCAAACTATACATTCCTAAGCAGGC 241
 1291 AACTGAGACTCATCTCAATGGAGATTTGGTGTCTTGCAGATCCATGTTCCCAAGGAAGC 1350
 242 ATACAGATGAGCTTCTGTTGTTTTTAACGACACACACGCTATGAAATAATAACATAA 301
 1351 ATACAGGCTGATTTGTTGTTTTTAATGACACAGATGCTTAAGACAACTATGATGAAA 1410
 302 TGATTTCTGATGATCAATAGAAAGCACCATGATGAAAAATTTATTTGAGGATTTCTTGGC 361
 1411 TGACTTCAGTATACCTGTAAGAGTGTGTATGCAATCATTTGACTTTGAAAAATTTCTTGT 1470
 362 TGAAGAAAGCAACGAACTTTGAGACCTTGGCAATGAGGAGCTGAAAGGAGGAGACA 421
 1471 TGAGGAGAAATGGAGAGAACAGGAGAACTTTGCTAAAGAACAACTGAAAGAGAAAGACT 1530
 422 AACTGATGAGCAGCGCGAATGGAGGAGAAAGGCGCGACATAAAGCTGACAGGATACA 481
 1531 AGGAGAGAACAAAGACGAATAGAGCAGAGAAAGCTGAATGGAAGCTGACAGGACACA 1590
 482 AGCCAAGGTTTGAGGTAGAGACGAAGAAATTAATTTGTCATGATTTTGGGTTTAGCCAG 541
 1591 AGCAAGGAGAGGCTGCAGAGAAAGAAAGATTTGCGAGAAATGATGTTGAAAGGCCAC 1650

QY 542 AGCTCCTGTGTATATTTATGTGTACATTGAGCCCATCAGACTGACAGAGAGGCTACTGT 601
 DB 1651 GAAGACTCGTGAATATCACCCTGGTACATAGAGCCAGTGAATTTAATGCGAGGACRAGGT 1710
 QY 602 CAGATTGTATTATAACATAAACTCAAGACCTCTAGTTCAAGTACTGAGATATGATGCA 661
 DB 1711 CAGGTTATACTATAACAAAAGTTGAGGTCCTCTCCCATGCTAAGGACTTGTGGATCCA 1770
 QY 662 TGGTGGCTATACAAATTTGGATTGATGGACTCTCTTTGCTGGAAGGCTTGTTCATCATCA 721
 DB 1771 CCGAGGATATAATAATTTGGAAGGATGGTTGCTATTGTCAAAAAGCTTGTTAATCTGA 1830
 QY 722 TGACAAAGATTGTGATTGTTGTTGTCAGATGTTGTCGTCCTGAAAGAACATATGTATT 781
 DB 1831 GAGAAATAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1890
 QY 782 GGACTGGGTTTTGCTGACGGCCACAGGGAGTGCAGAGAAATTAATGACAAATGGAGG 841
 DB 1891 GGATTGGGTTTTGCTGATGGTCCACCCAAAGCATGCCATTGCTTATGATAACAATCACCG 1950
 QY 842 ACATGATTTTCATGCTACCCCTTCCAAATAACATGACTGAGGAGAGATATTGATGGAAGA 901
 DB 1951 CCAGACTTCCATGCCATTTGTCCTCCCAACCAATCCGAGGAAATTAATGGTTGAGGA 2010
 QY 902 AGAACAAAGGATCTATACAAAGCTTCAACAGAGAGGAGGAGGAGGAGGCTATTAA 961
 DB 2011 AGAACATCAGATCTTTAGACACTTCAGAGAGAGAGAGGCTTAGAGAGGCTATGCG 2070
 QY 962 AAGGAGGCTGAGAGAAATGCAAAAATGAAAGCTGAGATGAGAGGAGGAGGAGGCTATGAAAT 1021
 DB 2071 TGCTAAGGTTGAAAAAACAAGCACTTCTGAAAACTGAAAAAGGAAAGAACTATGAAATC 2130
 QY 1022 GTTCTGGTTTTCTCAGAAACACATTTGTTACACCGAACCACTTGAATATACATCTGCAAC 1081
 DB 2131 ATTTTACTGTCTCAGAGCATGTAGTATATCTGAACTCTTTGATATCCAGCTGAAG 2190
 QY 1082 TACTATTGATGCTTTTATAATCCCTTCTAATACAGTTCTAACTGGAAGGAGGAGGTTG 1141
 DB 2191 CAGGCTCAGTTTACTATTAATCCGCCCAATACAGTACTTAATGGTAAACCTGAAATTTG 2250
 QY 1142 GTTTCGATGTTCCCTTAAATCGTTGGATGATTCAGGTGGGTTGCTCCACCTCAGAAAT 1201
 DB 2251 GTTCAGATGTTTCAATTAATCGCTGGACTCACCGCTGGTCCATTTGCCACCTCAGAAAT 2310
 QY 1202 GGTAACAGAGAAATGGTTTACACCTAAAGCAACAGTTTACGTTCCAGAGATGCTA 1261
 DB 2311 GTCGCTGTGAAATGGCACCCATGTCCAGAGCACTGTGAAGGTTCCATTTGGATGCTA 2370
 QY 1262 TATGATGGACTTCGTTTCTCGGAGTCAAGAGAGGTTGGAATTTATGATAACAGAAATGG 1321
 DB 2371 TATGATGGATTTTGATTTTCCAGAGAGAGATGTTGGGATTTTGGACAAATAGAGCGG 2430
 QY 1322 GTTACGATATCATATTCCTGTTTGGGTCAATTCGAAGGAGGAGGAGGAGGAGGAGGAGG 1381
 DB 2431 AATGAGATATCATATCTGTTTGGAGGAGTCCGCTAAAGAAACCTCCAAATGATATGT 2490
 QY 1382 CCACATGCTGTTGAGATGGCACAATCGCAAGGTTGGAGGCTTGTGATGTTGTAC 1441
 DB 2491 CCATATGCTGTGAAATGGCACCAATTCGAAGGTTGGAGGAGGAGGAGGAGGAGGAGGAG 2550
 QY 1442 TAGTCTTTTCACTGCTGTGCAAGATTTAGGACAAATGTGGAGGTTATTTCTTCAAAAGTA 1501
 DB 2551 TAGTCTTTCCGTTGCTGTTCAAGATTTAAACCAATATGTTGATATTTATCTTACCTAAGTA 2610
 QY 1502 CGTTTGTCTGAATCTAAGCAATGTCAAGATCTCAAAATCCATCAGATTTTCTTGGGG 1561
 DB 2611 TGACTGTTTCAAGATGAATTAATGTGAAGGACTTTCGGTTTTTCAAAAAAAGTACTTTTGGGG 2670
 QY 1562 TGGTCTGAAATTAATGTTGGGCTGGAGTGTAGTGGAGGCTTGTGTTTACTTCTCTGGA 1621
 DB 2671 TGGGACTGAAATTAAGTATGGTTTGGAAAGGTTGGAAAGGTTCTTCGGTCTATTTTTTGGGA 2730

1622 ACCTCAAAATGGGATGTTGGAGTCGGATATGATGATG---GCAGGAGCATGACCGCG 1678
 Db GCCTCAAAACGGGTATTTTCGAAAGGGTGGCTCTATGGTTGTAGCAACGATGGTGAACG 2790
 1679 ATTTGGCTCTCTGCTGCTCTCTCTAGAGTTCTCTCTCAAGTGGATCTCTCTCGAA 1738
 Db ATTTGGTTCT 2850
 1739 CATATACATGTCATGATGTTGGTCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1798
 Db TATCATTCATTCATGATGTTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2910
 1799 CGGAGTCTAGCTTGGCAACCGAGGGTGTATTCACCATCCACATCTCTCTCTCTCTCT 1858
 Db TACACACTATGGTCTAGCAAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2970
 1859 AGCGCATCATATTGGCAAAAGCAATGAGATATGATATAGCAAACTCTCTCTCTCTCT 1918
 Db GGAGATCTCTATTGGGAGAGCAATGATCTACGAGACAAAGCTCTACACAGTTTCAACCA 3030
 1919 ATATTCAAAGGAAGTGTGAGTCTATGTCGATAGTTCCTCTCTCTCTCTCTCTCTCTCT 1978
 Db TTACTCACAGGAGGTGTCTGAAACCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3090
 1979 CATCTCAATGGAAATGATCCGGATATATGGATCCGTACAAATGACAACTTTATCCCGGT 2038
 Db TATAGTGAATGGGATGACCCAGATATTTGGGATCTCTCTCTCTCTCTCTCTCTCTCTCT 3150
 2039 CCATCTACACTTGTGAGATGTTGGTGAAGCAAGAGGCTCTCTCTCTCTCTCTCTCTCT 2098
 Db TCCGTACATCTCAGAAACGTTGTTGAGGCAAAACAGCAGCCAGGAGCTTTGACGCG 3210
 2099 GAATTTGGTGTACAGCAAAATGATGATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2158
 Db AAAACTTTGGACTGAAACAGGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3270
 2159 CCAAAAGGGATCTCACTGATCAAGATGCGATTCACCGTACACTCGAAACGGAACGACA 2218
 Db CCAGAAAGGAATCCACTCTCATTAACATGCTATTTGGCGACCTTTGGACGGAACGACA 3330
 2219 GGTGGTTTGTCTGTTGCTCAGCGCGGACTCTCGAATCCAAAGCTGATTTTGTCAACCTGG 2278
 Db GGTAGTCTTGTCTGTTCT 3390
 2279 GAATAGCTTCAACGGCTGTAACCATGGGCAAGTGAAGGCTTCTCTCTCTCTCTCTCTCT 2338
 Db AAATCAATTTGCACTCCAAATATATGATGACCGGCAAGCTCTCTCTCTCTCTCTCTCT 3450
 2339 TCTCTCGCATCTGATATACGCTGGCTCTGACTTCATTCTGCTCTCTCTCTCTCTCTCTCT 2398
 Db ACTTTCTCACTGATATATGCTGGTCTGATTTTATTTCTAGTCTCTCTCTCTCTCTCTCT 3510
 2399 TTGGCGCTTAACTAGCTGTCTGCTCCCATGCGGATATGAAACCATTCGATTTGCTCCG 2458
 Db ATGTGGAATCAACAACTTACCGCTATGAGATATGTTTCAATTCAGTCTCTCTCTCTCT 3570
 2459 TGGAGGCTTCTCGACACTGTCTCTGATGTGACATGACAGGAGACGAGCCGAGATCG 2518
 Db TGGAGGACTTTATGATGATCTGATTTGATGTTGACCATGACAAAGAGAGAGCAACAGTG 3630
 2519 AGGCTTGAAGCCCAACGGGTTTATGCTTTTACCGGAGCTGATAGCAACGGTGTGACTAG 2578
 Db TGGTCTTGAACCAATGGATTCAGCTTTGATGAGGAGATGCTGCGGAGTGTATATGTC 3690
 2579 GCTGAACAGGGGATCTCAG 2598
 Db TCTGAATAGAGCTCTCTCTG 3710

RESULT 10
 ADA68321
 ID
 ADA68321 standard; DNA; 3078 BP.
 XX

AC ADA68321;
 XX 20-NOV-2003 (first entry)
 XX Arabidopsis thaliana gene, SEQ ID 816.
 XX Plant; bacterial infection; fungal infection; viral infection; ds.
 XX Arabidopsis thaliana.
 XX W02003000898-A1.
 XX 03-JAN-2003.
 XX 22-JUN-2001; 2001WO-1B001105.
 XX 22-JUN-2001; 2001WO-1B001105.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.
 XX Identifying at least one gene involved in plant resistance or response to
 XX pathogenic infection for conferring resistance or tolerance to a plant to
 XX bacterial, fungal or viral infection by determining or detecting plant
 XX gene expression.
 XX Claim 6; SEQ ID NO 816; 899pp; English.
 XX The present invention relates to a method (M1) for identifying genes
 XX involved in plant resistance or response to pathogenic infection. M1
 XX comprises identifying a gene whose expression is significantly altered in
 XX the incompatible interaction of plant gene expression relative to
 XX expression of the gene in an uninfected plant, in a mutant plant that
 XX does not express a gene associated with response to pathogenic infection,
 XX or in a corresponding incompatible or compatible interaction. (M1) is
 XX useful for conferring resistance to resistance or tolerance to a plant to
 XX bacterial, fungal or viral infection. The present sequence was used to
 XX illustrate the invention.
 XX Sequence 3078 BP; 946 A; 535 C; 763 G; 834 T; 0 U; 0 Other;
 Query Match 43.9%; Score 1141.2; DB 7; Length 3078;
 Best Local Similarity 65.7%; Pred. No. 0;
 Matches 1719; Conservative 0; Mismatches 878; Indels 21; Gaps 3;
 QY 2 GCTTGTCTGAAAAAATTTATTCGCTGGGAAACAAAGTTGTTTACTTATCCAGATGATTTGAA 61
 Db 342 GCTTGCAGCGAAAAATTTGGCGAGAGGTGATAGAATGTTTGTGTATCCCGTTATTTGTAA 401
 QY 62 AGCTGATTCACAAATGATCTCTATTTCATTCGTGATCTATCAGTGTGGCCAAATGAGCC 121
 Db 402 ACCTGATGAAGACATAGAAGTGTTCCTCAACAGGAATCTGTGACTCTGAATACGAAC 461
 QY 122 TGATGTACTTATCAAGAGGACATTCATCGGTGGAGTGGAGATTTTTCACCTGAAAAATTT 181
 Db 462 CGATGTTTTGATCATCGGGGGCTTTTAAAGATGAGATGGAAGTCTTTCACAGAGATTT 521
 QY 182 GCACAAGAGCGAGCTGGCAGGGGAGCTGGTGGTCTGCAAACTATACATCTCTTAAGCAGCC 241
 Db 522 GGAAAGACCTGGATCCATGAAGATTTGTTGTCATGCTCTCTCTATATCCCAAGAAAGC 581
 QY 242 ATACAGATGAGCTTTGTTGTTTTTAACGGACACACGGTATATGAATATATAACAATAA 301
 Db 582 GTATAAGATGAGCTTCTGTTTTCATTCATGGGCAAGTGTATATGACACAAATGATCTCAA 641
 QY 302 TGATTTCTGTATACAAATAGAAAGCACCATGATGATAAATTTATTTGAGGATTTCTTGGC 361
 Db 642 AGATTTTGTGTAGATATAAAGGTTGGATGATGATTAAGTTGATTTGAGATTTCTTCT 701

362	Y	TGAGNAAGCAACGAGAACTTCGAGAACCTTGCAAATGAGGAAGCTGAAAGGAGGAGACA	421
702	b		761
422	Y		481
762	b		821
482	Y		541
822	b		881
542	Y		601
882	b		941
602	Y		661
942	b		1001
662	Y		721
1002	b		1061
722	Y		766
1062	b		1121
767	Y		826
1122	b		1181
827	Y		886
1182	b		1241
887	Y		946
1242	b		1301
947	Y		1006
1302	b		1361
1007	Y		1066
1362	b		1421
1067	Y		1126
1422	b		1481
1127	Y		1186
1482	b		1541
1187	Y		1243
1542	b		1601
1244	Y		1303
1602	b		1661
1304	Y		1363
1662	b		1721
1364	Y		1423
1722	b		1781
1424	Y		1483

1782	Db	CCTAGGTTGAU GTTGTCAC TAGTCTAT CTCGCGCTCTTCAAGAA TTAAACCA TAATGTGGGA	1841
1484	Qy	GGTTATTCTTCCAAAGTACGGTTGGTTGGA CTTAAGCAATGTCAAGAA TCTACAAATCCA	1543
1842	Db	TATAGT TTTTCCAAAGTATGAT TGATTAAGCACA AATTTTGTGAAGGAC TTGCAATTTAA	1901
1544	Qy	TCAGAGTT TTCTTGGGGTGGTTCTG GAATAAAT GTGTGGCGTGGACTAGTCCGAAGCCCT	1603
1902	Db	CAGAAGCTATC ACTGGGAGGAC TGAATAAAG TTTGGCATGGAAAAAGTAGAAGSCCT	1961
1604	Qy	TTGTCTTTACT TCTCTGGAACCTCA AAATGGGATGTTTGGAGTCGGATATGTATATGGCAG	1663
1962	Db	TTCGGTTTACT TTTAGATCCAA AAATGGATTTTTCACGGAGGATGTGTTTACGGTTG	2021
1664	Qy	--- GGACGATGACCGCGATTTTGGCTTCT CTGTCTGTCTCTGTCTAGAGTTCTCTCTCCA	1720
2022	Db	TGCAGATGATG CAGGAAGATTCGGTTTCT CTGTCATGCGGCTCTTGAATTTCTTCTCCA	2081
1721	Qy	AAGTGGATCTTCT CCGAACAATA ATCA TTGCCATGATTTGGTCAAGTCTCTCTGTGGCTG	1780
2082	Db	AGSAGGT TCCATCCAGACAT TCTTCACTGTCTATGACTGTCTAGTCTCTCGGTTTCATG	2141
1781	Qy	GGTACAAAGGAA A CTACGGAA GTCTAGCTTGGCAAC CGCAGGGTGGTATTCA CCAT	1840
2142	Db	GTTATTCAAGGATCAT TACACAGTACGGT TTAA TTAAACCCGTA TGTCTTCA CAT	2201
1841	Qy	CCACAATCTTGAA TTTGGAGCGCAT CATATTTGCCAAAGCAATGAGATATTTGTATGAAGC	1900
2202	Db	TCATAATTTGGAATTTGGAGCGAATGCCAT TGGTAAAGCAATGACATTTGCAGACAAAGC	2261
1901	Qy	AACAAC TGTCTTAATPACAT PATTCAAAGAA GTGTCAAGTCCGATATATGGGATCCGTACAA	1960
2262	Db	CACAACGGTTTCCAACT TATGCTTAGGAAGTTGCTGGAAACTCTG PAA TCTCTG CACA	2321
1961	Qy	TC TTGGGAAT CTATGGCA TCTCAATGGAA TTGATCCGATATATGGGATCCGTACAA	2020
2322	Db	TTTATACAA TTTTCACGGAA TTAAACGGGATTTGACCAGATATATGGGATCCATATAA	2381
2021	Qy	TGACAAC TTTATCCGGTCCACTAC CTTGTGAGATGTGGTTGAAGCAAGAGGGCTGC	2080
2382	Db	CGATAC TTTATCCCGTAC CTTATCTTACAGAA CGTTGTAGAAAGCAAAAGACAGC	2441
2081	Qy	TAGAGGGCACTG CAGCAGAA GTTTGGTTACAGCAATCCGATGTCCCGTCTGTAGGAAT	2140
2442	Db	CAAGGAAGAATTG CAAAACAGGCTTGGACTAAAGATGCCGATTTTCA GTAGTAGGAT	2501
2141	Qy	CGTCACTCGCTG CAGCCCAAAAGGGATCC ACTGTATCAAGCATCGATTCACCGTAC	2200
2502	Db	TATTTACGGCTTAA CACACAGAGGGAATACATTTGATCAAGCAGCTATTTGGCGTAC	2561
2201	Qy	ACTCGAACGGAACG GACAGGTGTTTGGTTTGGTTCAGCGCGGATCTTCGATCCAAAGC	2260
2562	Db	CTTGGAAACGGAATG GACAGGTGTCTTATTAGTTTCAGCTCCAGATCCTCGGATCCAAA	2621
2261	Qy	TGATTTTGTCAACCTG CGGATACGCTCCACGGCGTAAACCATGGCAAGTAGGCTTTC	2320
2622	Db	TGATTTTGTAAACTTGGCAAAACCAAT TACATCTTCTCATGTCGACCGGCTCGCTGT	2681
2321	Qy	CTTGACCTTAC CAGCAGCCTCTCTCGCATCTGATATACGCTGGCTCTGACTTCA TCTGCT	2380
2682	Db	TCTAACCTAC GATGAACCTCTTTCCCATTTGATTTATGCTGGGGCTGACTTTATTCTTGT	2741
2381	Qy	CCCATCTATATTTGAGCCTTGGGCTTA CTCAGCTCGTCGCCATGCGGTATGGAAACCAT	2440
2742	Db	ACCGTCGATATTTGAGCCATGTGGACTGACACAGCTCATAGCCATGAGATACGGCGCTGT	2801
2441	Qy	CCCGATTCGCGCAAGACTGGAGGCTCTTCGACACTGTCTTCGATGTGTGCAATGACAA	2500
2802	Db	TCTCTGTTGTAGAAAACTGGAGGACTCTTTGATACGGTTTTTGTATGTTTACCAACGATAA	2861
2501	Qy	GGAACGAGCCGAGATTCGAGGCCCTTGACCCAAACGGGTTTAGCTTTGACGGAGCTGATAG	2560

XX WPI, 2000-647602/62.

XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and WST-II,
XX PPT useful in modifying plant starch content and/or composition.

XX Claim 1; Page 187-188; 21pp; English.

PS The present invention relates to novel protein and coding sequences from
XX wheat. The proteins are wheat starch synthases, designated SSII and
XX SSIII. These can be used in the modification of plant starch content or
XX composition, and to screen plants to identify mutations which affect
XX starch content and composition. The starch can then be used in food
XX products, such as flour, and in films, coatings, adhesives, building
XX materials and packaging materials

XX Sequence 2446 BP; 780 A; 400 C; 624 G; 642 T; 0 U; 0 Other;
XX SO

RESULT 12	
AAC86416	
ID AAC86416 standard; DNA; 2446 BP.	
XX	
AC AAC86416;	
XX AC	
DT DT	
XX 01-MAR-2001 (first entry)	
XX	
DE Wheat starch synthase III gene fragment SEQ ID NO: 12.	
XX	
XX Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;	
KW food product; adhesive; ds.	
KW	
XX Triticum sp.	
OS OS	
XX WO20006745-A1.	
FN FN	
XX	
XX 09-NOV-2000.	
XX	
XX 28-APR-2000; 2000WO-AU000385.	
PF PF	
XX 29-APR-1999; 99AU-000000052.	
PR PR	
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.	
PA (GOOD-) GOODMAN FIELDER LTD.	
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	
PA	
XX Morell M. Li Z. Rahman S. Appels R;	
PI	

[illegible]

PA	(ALLEN S M.	AC	AAD33324;
PA	(BECK/) BECKLES D M.	XX	
PA	(THOR/) THORPE C J.	DT	01-JUL-2002 (first entry)
XX		DE	Rice starch synthase D1U homologue cDNA #1.
PI	Allen SM, Beckles DM, Thorpe CJ;	XX	Rice; starch synthase; D1U; enzyme; transgenic plant; genetic mapping;
XX		KW	starch synthesis; gene; ss.
XX		XX	Oryza sativa.
DR	WPI: 2002-291589/33.	OS	
DR	P-PSDB; AAE20907.	XX	
XX	Novel isolated starch synthase D1U homolog polypeptide and polynucleotide	Key	Location/Qualifiers
PT	which is useful for transforming a cell and producing a transgenic plant	FT	7..357
PT	having altered level of starch synthesis and carbohydrate composition.	FT	/*tag= a
XX		FT	/product= "Rice starch synthase D1U homologue protein"
XX		FT	/note= "CDS does not include start and stop codon"
PS	Claim 8; Page 15; 18pp; English.	FT	/partial
XX		FT	
XX	The invention relates to isolated starch synthase D1U homologue	XX	US2002029394-A1.
CC	polypeptides and their polynucleotides. The polynucleotide is useful for	XX	07-MAR-2002.
CC	transforming a cell and for producing a transgenic plant by transforming	XX	18-DEC-2000; 2000US-00739438.
CC	a plant cell with the polynucleotide and regenerating a plant from a	XX	22-DEC-1999; 99US-0171514P.
CC	transformed plant. The polypeptide is useful for preparing antibodies.	XX	(ALLE/) ALLEN S M.
CC	The polynucleotide is useful as probes for genetically and physically	XX	(BECK/) BECKLES D M.
CC	mapping the gene that they are a part of, and as markers for traits	PA	(THOR/) THORPE C J.
CC	linked to those genes. The polynucleotide is useful for creating	XX	
CC	transgenic plants in which the polypeptide is present at higher or lower	XX	Allen SM, Beckles DM, Thorpe CJ;
CC	levels than normal or in cell types or developmental stages in which they	XX	
CC	are not normally found, for altering the level of starch synthesis and	XX	WPI: 2002-291589/33.
CC	carbohydrate composition in the plants, and to design and produce primers	DR	P-PSDB; AAE20906.
CC	or probes. The present sequence is rice starch synthase D1U homologue	XX	
CC	cDNA	XX	Novel isolated starch synthase D1U homolog polypeptide and polynucleotide
XX		PT	which is useful for transforming a cell and producing a transgenic plant
XX		PT	having altered level of starch synthesis and carbohydrate composition.
XX		XX	Claim 8; Page 14; 18pp; English.
XX		XX	The invention relates to isolated starch synthase D1U homologue
CC	polypeptides and their polynucleotides. The polynucleotide is useful for	CC	transforming a cell and for producing a transgenic plant by transforming
CC	a plant cell with the polynucleotide and regenerating a plant from a	CC	transformed plant. The polypeptide is useful for preparing antibodies.
CC	The polynucleotide is useful as probes for genetically and physically	CC	mapping the gene that they are a part of, and as markers for traits
CC	linked to those genes. The polynucleotide is useful for creating	CC	transgenic plants in which the polypeptide is present at higher or lower
CC	levels than normal or in cell types or developmental stages in which they	CC	are not normally found, for altering the level of starch synthesis and
CC	carbohydrate composition in the plants, and to design and produce primers	CC	or probes. The present sequence is rice starch synthase D1U homologue
CC	cDNA	CC	
XX		XX	Sequence 548 BP; 156 A; 121 C; 113 G; 155 T; 0 U; 3 Other;
XX		XX	Query Match 11.2%; Score 290.6; DB 6; Length 548;
XX		XX	Best Local Similarity 79.9%; Pred. No. 2.9e-75;
XX		XX	Matches 341; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY	1661 CAGGAGCATGACGCCGCGATTGGCTTCTTCGTCCTCTCTAGAGTTTCTCTCTCA 1720	QY	2191 TTCCACCGTACCTCGAACCGGACAGGTGGTTTGTGTTTGTTCAGCGCGGACTCTC 2250
Db	3 CAGCAATGACGAGAGTAGATTGGCTTCTCTGCTCTCTAGAGTTTCTCTCGGCA 62	Db	2 TTACACGAACCTCTTGAACGCAATGGGCGAGTGGTTTGTCTAGGCTCAGCTCCGATCATC 61
QY	1721 AAGTGGATCTTCTCGAATATATACATTCGATGTTCAAGTGTCTCTGTTCCTG 1780	QY	2251 GAATCCAGCTGATTTTGTCACTCGCAATACGCTCCACGCGGTAAACCATGGGCAAG 2310
Db	63 AAATGGATCTTCTCTGATATATATATATGTCATGATTTGGTCAAGTGTCTCGAGTTGCTG 122	Db	62 GCATACAAAGGTGACTTTTACCACTTAGCTAGTAACTGCATGCGAATACCATGTCGTG 121
QY	1781 GCTACACAGGAAACTACGGAAGTCTAGCTTGGCAACGACGCGGTGTTTACCAT 1840	QY	2311 TGAGGCTTCTCTGACCTAGCAGGAGCTCTCTCGCATCTGATATACGCTGGCTCTGACT 2370
Db	123 GCTATTCAGGAAACATATGCTCAAAATGGACTGTCAAAATGGCGGGTGTATTACCAT 182	Db	122 TAAAGCTTTGTTTAACTATGATGAGCCACTATCTCATTTGATTTATGCTGTCGCGACT 181
QY	1841 CCACATCTTGAATTGGAGCGCATCATATTGGCAAGCAATGAGATATTGTGATAAGC 1900		
Db	183 CCACAACTTGAATTGGTGCATCATACATCGCAAGCAATGGACGTTGTGATAAGC 242		
QY	1901 ACAACTGTCTTAATACATATTCAAGGAAGTGTCAAGTGTGTCATGTCATAGTTCTCA 1960		
Db	243 TCAACTGTCTTAATACATATTCAAGGAAGTGTCAAGTGTGTCATGTCATAGTTCTCA 302		
QY	1961 TCTTGGAAATCTATGGCATTTCTCAATGAAATGATTCGGATATATGGAATCCGTACA 2020		
Db	303 CTTTCTCTANTCCACGGTATTCTGTAAGCAATGATTCAGATATTTGGGATCCATACAG 362		
QY	2021 TGACAACTTTATCCCGGTCACTACACTGTGAGATGTGTTGAAGGCAAGAGGCTGC 2080		
Db	363 TGACAACTTTATCCCGGTCCACTATACCTCTGAGATGTGTTGAAGGCAAGAGTGTGCTGC 422		
QY	2081 TAAGAGG 2087		
Db	423 CAAAGAG 429		
RESULT 15			
AAD33324			
ID	AAD33324 standard; cDNA; 437 BP.		
XX			

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 05:03:49 ; Search time 211 Seconds
(without alignments)
6832.997 Million cell updates/sec

Title: US-10-634-262-1_COPY_2425_5022

Perfect score: 2598

Sequence: 1 agctgtgtaaaaaattat.....gctgaacagggcgtctcag 2598

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2598	100.0	6027	2	US-08-968-542C-1	Sequence 1, Appli
2	2598	100.0	6027	4	US-09-554-467A-1	Sequence 1, Appli
3	1500.4	57.8	4121	4	US-09-638-524A-1	Sequence 1, Appli
4	1204.8	46.4	4168	3	US-08-836-567-11	Sequence 11, Appli
5	1204.8	46.4	4168	4	US-09-606-304-11	Sequence 11, Appli
6	931	35.8	2303	3	US-08-836-567-1	Sequence 1, Appli
7	931	35.8	2303	4	US-09-606-304-1	Sequence 1, Appli
8	175	6.7	212	4	US-09-313-294A-101	Sequence 101, App
9	145	5.6	2652	3	US-09-115-704-1	Sequence 1, Appli
10	145	5.6	2652	4	US-09-780-115-1	Sequence 1, Appli
11	144.8	5.6	3434	4	US-09-388-743-9	Sequence 9, Appli
12	111.8	4.3	2380	1	US-08-572-951-3	Sequence 3, Appli
13	85.6	3.3	2097	3	US-08-941-445A-10	Sequence 10, Appli
14	83.6	3.2	1248	4	US-08-489-039A-3687	Sequence 3687, Ap
15	83.6	3.2	1536	4	US-09-489-039A-3862	Sequence 3862, Ap
16	77.4	3.0	2202	4	US-09-388-743-1	Sequence 1, Appli
17	74.4	2.9	2825	4	US-09-196-390-5	Sequence 5, Appli
18	72.6	2.8	7218	1	US-08-232-463-14	Sequence 14, Appli
19	69.6	2.7	1798	4	US-09-345-214-16	Sequence 16, Appli
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22	69.6	2.7	2019	4	US-09-743-980-15	Sequence 15, Appli
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24	69.6	2.7	2248	4	US-09-743-980-20	Sequence 20, Appli
25	67.2	2.6	2176	4	US-09-388-743-13	Sequence 13, Appli
26	67	2.6	1464	1	US-07-733-085-1	Sequence 1, Appli
27	67	2.6	1464	1	US-08-469-202-11	Sequence 11, Appli

28	67	2.6	1464	2	US-08-484-434C-11	Sequence 11, Appli
29	67	2.6	1464	4	US-09-384-361-11	Sequence 11, Appli
30	66.8	2.6	2067	4	US-09-388-743-21	Sequence 21, Appli
31	66	2.5	2239	4	US-09-196-390-1	Sequence 1, Appli
32	65.6	2.5	2542	3	US-08-941-445A-6	Sequence 6, Appli
33	63.2	2.4	1230025	4	US-09-198-452A-1	Sequence 1, Appli
34	62.6	2.4	1650	4	US-09-252-991A-8097	Sequence 8097, Ap
35	62.6	2.4	2145	4	US-09-252-991A-8205	Sequence 8205, Ap
36	62	2.4	1818	4	US-09-731-166-3	Sequence 3, Appli
37	62	2.4	2267	4	US-08-679-645-25	Sequence 25, Appli
38	61.4	2.4	1601	3	US-08-735-491-1	Sequence 1, Appli
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44	57	2.2	1528	4	US-09-345-214-6	Sequence 6, Appli
45	57	2.2	1528	4	US-09-743-980-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-968-542C-1
; Sequence 1, Application US/08968542C
; Patent No. 5981728
; GENERAL INFORMATION:
; APPLICANT: Myers, et al.
; TITLE OF INVENTION: dulli Codes For A No. 5981728el Starch
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77071

parent

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0.1 for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,542C
FILING DATE: No. 5981728ember 12, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D6036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6027 bp
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: cdna to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: maize
TISSUE TYPE: endosperm
IMMEDIATE SOURCE:
LIBRARY: maize endosperm cdna library in

LIBRARY: gtl11
CLONE: pMgf10; pMg6Aa; pMgt6-2M
US-08-968-542C-1

Query Match 100.0%; Score 2598; DB 2; Length 6027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-554-467A-1
; Sequence 1, Application US/09554467A
; Patent No. 6639125
; GENERAL INFORMATION:
; APPLICANT: Myers, Alan M.
; APPLICANT: James, Martha G.
; TITLE OF INVENTION: dullel Coding for a No. 6639125el Starch Synthase and Uses
; FILE REFERENCE: D6036PCT
; CURRENT APPLICATION NUMBER: US/09/554,467A
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/24225
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/062,102
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 1
; LENGTH: 6027
; TYPE: DNA
; ORGANISM: maize
; FEATURE:
; OTHER INFORMATION: cDNA sequence corresponding to the gene encoding the
; OTHER INFORMATION: starch synthase enzyme DUL.
US-09-554-467A-1

Query Match 100.0%; Score 2598; DB 4; Length 6027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-09-638-524A-1
; Sequence 1, Application US/09638524A
; Patent No. 6590141
; GENERAL INFORMATION:
; APPLICANT: Aventis CropScience GmbH
; TITLE OF INVENTION: Nucleic Acid Molecules from Plants Encoding Enzymes
; FILE REFERENCE: 514413-3833
; CURRENT APPLICATION NUMBER: US/09/638,524A
; PRIORITY FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 19 937 348.5
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4121
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (442)..(3954)
US-09-638-524A-1

Query Match 57.8%; Score 1500.4; DB 4; Length 4121;
Best Local Similarity 74.4%; Pred. No. 0;
Matches 1934; Conservative 0; Mismatches 601; Indels 63; Gaps 1;

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Db 1358 AGGCTGATTGATGATGATGATCTTTACTTTAAACCGCAGCATGTGCGGCTTAGCTAGT 1417
QY 121 CTGATGTACTTATCAAGAGCATTTCAATGGTGGAGTGGAGATTTTCTACTGAAAAAT 180
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Db 1538 CATACAGACTAGACTTTGTATTTCTTAACGGTGACACTGTCTATGAAATAACAATCACA 1597
Qy 301 ATGATTTTCGTGATACAAATAGAAGCACCATGATGAATTTATTTGAGATTTCTTGG 360
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Qy 361 CTGAAGAAAAGCAACGAGAACTTGAGAACCTTGCAAAATGAGGAGCTGAAAGGAGGAGAC 420
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Qy 601 TCAGATTTGATTAATACATAACTCAAGACCTCTAGTTTCAAGTACTGAGATATGAGATGC 660
Db 1898 TTAGATTTGATTAATAGAGCTCGAGATCACTAATGCAATAACACTGAGATTTGGATGC 1957
Qy 661 ATGTGGCTATAACAAATTTGATGATGACTCTCTTTTGTGAAAGGCTTGTTCATCATC 720
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Qy 1681 TTGGCTTCTTCTGCTGTTCTAGAGTTTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1740
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Qy 1801 CGAAGTCTAGTTTGGCAACGCGACGGGTGATTTACACATCCCAATCTTTGAATTTGGAG 1860
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Qy 1981 TTTCTCAATGGAATTTGATTCGGATATATGGGATCCGTACATGACAACTTTATCCCGTCC 2040
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TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4168 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to RNA
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
STRAIN: cv. D, sir, e
TISSUE TYPE: leaf tissue
IMMEDIATE SOURCE:
LIBRARY: cDNA-library in Lambda ZAPII
OTHER INFORMATION: CDS
FEATURE:
LOCATION: 307..3897
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-606-304-11

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DB 1236 ACCTGATGAAGATGTCGAGATATTTCTTAAACAGAGGTCCTTCCACTTTGAAGAAATGAGTC 1295

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DB 1896 GAGATAGATGGTANTGGTGTATACAGAGTTGTTTATTCCTGATCAGGACATTTCTT 1955

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/   HYPOTHETICAL: NO
/   ANTI-SENSE: NO
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/     STRAIN: cv Berolina
/     TISSUE TYPE: tuber tissue
/   IMMEDIATE SOURCE:
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/   FEATURE:
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/     OTHER INFORMATION: /function= "Polymerization of starch"
/     /product= "starch synthase"
/   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-606-304-1

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Best Local Similarity 68.5%; Pred. No. 2.2e-284;
Matches 1301; Conservative 0; Mismatches 595; Indels 3; Gaps 1;

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DB 13 AAAAGCTTGTAAATCTGAGAGAAATAGATGGTGGTGGTATACAGAGGTTGTATTTC 72

QY 763 CTGAAGAAACATATGATTGGACTGGGTTTTTGTGCTGACGGCCACACAGGAGTGCAGGA 822
DB 73 CTGATCAGGCACCTTCTTGGATTGGGTTTTTGTGCTGATGTTCCACCCAGCATGCCATG 132

QY 823 ATTATGACAAATGAGGAGCATGATTTTCATGCTACCTTCCAAATAACATGACTGAGG 882
DB 133 CTTATGATAACAATCACGCCAAGACTTCCATGCCATTGTCCCAACCAACCATTCGGAGG 192

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DB 313 AGGAAAGAACTATGAAATCATTTTACTGTCTCAGAAAGCATGTAGTATATATCTGAGCCTC 372

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QY 1123 CTGGAAGCCAGAGTTGGTTTCGATGTTTCTTTAATCGTTGGATGTATCCAGTGGGG 1182
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Db 1982 GGAAGATGAACGATAC 1998
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; Patent No. 6617495
; GENERAL INFORMATION:
; APPLICANT: Koessmann, Jens
; APPLICANT: Proberg, Claus
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES FROM PLANTS CODING ENZYMES
; TITLE OF INVENTION: WHICH PARTICIPATE IN THE STARCH SYNTHESIS
; FILE REFERENCE: GFB-6 DIV
; CURRENT APPLICATION NUMBER: US/09/780,115
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 09/115,704
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: PCT/EP97/00158
; PRIOR FILING DATE: 1997-01-15
; PRIOR APPLICATION NUMBER: DE 196 01 365.8
; PRIOR FILING DATE: 1996-01-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2652
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(2213)
US-09-780-115-1
Query Match 5.6%; Score 145; DB 4; Length 2652;
Best Local Similarity 51.4%; Pred. No. 5.2e-35;
Matches 657; Conservative 0; Mismatches 470; Indels 150; Gaps 8;
QY 1370 TATGCAATGTCCATGCTGCTTCAGATGGCACCACCAATCGCAAGGTTGGAGGCTTGG 1429
Db 731 TTGACATTTGCCATAGCAGAGATGGCTCTCGCAAGGTTGGTGGCTGCG 790
QY 1430 TGATGTTGCTAGTCTTTCAGTCTGTGCAAGATTAGGACACAAATGTGGAGTTAT 1489
Db 791 AGATGTGATCTGTGCTTGGGAAGGCACTTCAAAAAGGGGACCTTGTAGAGATTAT 850
QY 1490 TCTTCCAAAGTAGGTTGCTTGAATTAAGCAATGTCAGAAATCTACAAATCCATCAGAG 1549

Db 851 TCTTCCCAATATGATTCATGATGAGCAGATACCAATAAATAAATCTTAAGGTTCTAGATGT 910
QY 1550 TTTTCTTGGGGTGGTTCTGAAAATAAATGT-----TGGCGTGGACTAGT 1594
Db 911 TGTGGTGAAGTCTTACTTTGAAGGAAATATGTTTGCACAAAGATATGGACTTGAACGT 970
QY 1595 CGAAGCCCTTGGTTTACTTCTCGAACTCAAAA-----TGGGATGTTTGGAGTCGG 1648
Db 971 TGAAGGCTTCCGGTCTACTTTTGAACCGCAACATCCAGGTAAGTTCTTCTGGAGGGC 1030
QY 1649 ATATGTATATGGCAGGAGCATGACCGC-----CGAATTGGCTTCTTCTGCTGTTCTGTCT 1705
Db 1031 ACAATACTACGAGAGCATGATCACTTCAACCTTTTTCGTACTTTAGCGGTGTGCACT 1090
QY 1706 AGAGTTTCTCTCCAAAGTGGATCTTCTCGAAATAATAATCAATTCGATGATTTGGTCAAG 1765
Db 1091 GGAATTGCTTTACCAATCTGGGAAAGAAAGTTGACATAATTTCACTGCACTGACTGGCAGAC 1150
QY 1766 TGCTCTGTTGGCTGCTACACAAAGAAACACTACGGAAGTCTAGCTTGGCAACGCAAG 1825
Db 1151 TGCATTTGTTGACCTCTTTTACTGGGATGTATATGCAAACTGGGCTTCAACTCAGCTAG 1210
QY 1826 GTGTGTTTACCCTCCCAATCTTGAATTT-----1856
Db 1211 AATTTGTTTACCCTGTCACATTTTGAATATCAAGGAATCGCTCCAGCTCAGACTAGC 1270
QY 1857 -----1856
Db 1271 ATATTGTGCTTGTATGTTGATCACCTGGATAGACAGAGAAATCGGGATAATTCACA 1330
QY 1857 ----GGAGCGCATCATATTGGCAAGCAATGATATTTGATAAAGCAACACTCTCTC 1912
Db 1331 TGGCAGAAATAATGTTTAAAGGTGCTGTTATATTTCCAACTTGTGCAACTGTATC 1390
QY 1913 TAATACATATTCAAAGGAAGTGTCAAGTCTATGTTGCTATGTTTCTTCTTCTT 1964
Db 1391 ACCAACATATGACAGAGAGTTGCTCAGAGGTGGCGGTGGCTCCAGAGATACACTCA 1450
QY 1965 -----GGGAATTTCTATGGCAATTCATGGAATGTATGATATATGGAATCC 2014
Db 1451 AGTGCACTCCAAAGAAATTTGTTGGAATCTTAAATGGCAATTGACACAGATATCTGGAATCC 1510
QY 2015 GTACATATGACAACTTTATCCCGTCCACTACACTTGTGAGAAATGTTGTAAGGCAAGAG 2074
Db 1511 GTCTACGATAGTTTCTCAAGTTCAATACA---GTGCTAATGATCTATATGGAAGTC 1567
QY 2075 GGCTGCTAAGAGGGCACT-----GCAGCAGAAGTTTGGGTTACAGCAAAATCGATGCTCC 2128
Db 1568 AGCAAAACAAAGCAGCTCTTAGGAAGCAGTTGAAGCTTGTCTCCACACAGCTTCTCAACC 1627
QY 2129 CGTCGTAGGAATCGTCACTCGCTGACAGCCCAAGGGGATCCACTGATCAAGCATGC 2188
Db 1628 ATTAGTTGGTTGCTATACGAGGCTAGTTCTCTCAAAAGGGGTGATCATCTCATCAGGATGC 1687
QY 2189 GATTCAACCGTACACTCGAACGGAACGACAGGTGGTTTGTGTTGTTGAGCGCGGACTC 2248
Db 1688 AATATATAAATAAATGAGTTGGTGGTCAATTTGTTCTGCTGGGTTCAAGTCCAGTACA 1747
QY 2249 TCGAATCCAGCTGATTTTGTCAACCTGGCGAATACGCTCCACGGCGTAAACCATGGGCA 2308
Db 1748 GCATATCCAGAGAGAGTT-----CGAGGGTATTGGGACCAATTTTCAGAAACACACAA 1801
QY 2309 AGTGAGGCTTCTTTCAGCTCAGAGCGCTCTCTCGCATCTGATATAGCTGGGTCTGA 2368
Db 1802 TGTGAGGCTGCTTTTGAAGTATGATGCTCTGGCACATATGATCTTTGACAGCATCAGA 1861
QY 2369 CTTCAATCTGGTCCCATCTATATTTGAGCTTGGCGCTTAACTCAGCTCGTCCGATGCG 2428
Db 1862 CATGTTCAATGTTCTTCTATGTTTGAACCATGTGGCTCTACTCAGATGTTAGTATGCG 1921
QY 2429 GTATGGAACCATCCGATTTGTCGCAAGCTGGAGGCTCTTTCGACACTGTCTTCGATGT 2488
Db 1922 ATATGTTCTGTGCCAGTTGTTTCGGAGAACCGCGGTTTGAATGACAGTGTCTTCGATTT 1981


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QY 2166 GGGATCCACTGATCAAGCATGCGATTCAACGTTACCTGACCTCGAACGGAACGACGAGGTGGTT 2225
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1633 GGGTNGAYATHATGCGNGAYGCGNATHCAVTGGATHGCGNGCARGAYGTCARYTNGTN 1692
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2226 TTGCTTGGTTTCAGCGCCGACTCTCGAATCCAACTGATTTTGCACCTGGCGGAATACG 2285
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1693 ATGYTNGNACNGG-----NMNGCNGAYTNGARGAYATGYTNMNGN 1737
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2286 CTCACCGCGTAAACCTAGGCAAGTGGAGGCTTTCTTTGACCTACGACGACCTCTCTCG 2345
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1738 TTYGARWSNGARCAWENGAYARGTNGNGCNTGGTNGGNTTWSGNTCNYTNGCN 1797
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2346 CATCTGATATACGCTGCTGATCTCATCTCTGCTGCCATCTATATTGAGCCCTTGGCGC 2405
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1798 CAYMGNATHACNGCGNGCNGAYATHYTNATGCGNWSNMNGNTTYGARCCNTGYGN 1857
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2406 CTAACCTCAGCTCGTCCGATCGGTATGGAAACCATCCGATTGTCCGCAAGACTGGAGGG 2465
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1958 YTNAYCARNTAYGCVATGCGNTATGCGNATATGCGNATGCGNATGCGNATGCGNATGCGN 1917
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2466 CTCTTCGACACTGCTTCGATGTCGACATGACAAAGGAACGAGCCGAGATCGAGGCTT 2525
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Db 1918 YTNMNGAYACNGTNGCNCNTTYGAYCCNTTYAAYGAYACNGGNTGNGTGGACNTTY 1977
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2526 GA 2527
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Db 1978 GA 1979
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RESULT 13
US-08-941-445A-10
; Sequence 10, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941.445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2097 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
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; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2097
; US-08-941-445A-10

Query Match 3.3%; Score 85.6; DB 3; Length 2097;
Best Local Similarity 52.6%; Pred. No. 3e-16;
Matches 246; Conservative 0; Mismatches 204; Indels 18; Gaps 2;

QY 2039 CCATCACTTGTGAGAAATGTGGTTGAAGGCAAGAGGGCTGTCTAAGAGGGCACTGCGACA 2098
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Db 1446 CAATCACTGTTTGGAGAGCTTGACACCGGACGCGAGCTGCAAGCGCCCTCGACGG 1505
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QY 2099 GAAGTTTGGGTTACAG---CAAAATCGATGTCCCGTCTGTAGGAATCTGCTACCTGCGCTGAC 2155
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1506 GCAGCTGGGCTGCGAGTCCGCGACGAGTGCACACTGATCGGGTTCATCGGGCGCTGGA 1565
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2156 AGCCAAAAGGGATCCACCTGATCAAGCATGGAATTCACCGTACACTCGAAGCGAAGCGG 2215
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1566 CCACCAAGAGGGCTGACATCATCGCGACGCGATCCACTGGATCGCGGGGAGGAGCT 1625
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QY 2216 ACAGTGTGTTTGTCTTGTGTTTCAGCGCGGACTCTCGAATCCAACTGATTTTGTCAAACCT 2275
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Db 1626 GCAGCTGCTGATGCTGGGACCGCGCGGCC-----GACCTGGAGGACAT 1670
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QY 2276 GGGGAATACGCTCCACGGCGTAAACCATGGGCAAGTGAAGGCTTCTCTTGACCTTACGACGA 2335
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Db 1731 GCCCTCGCGCACCGCATCAGCGCGGCGGAGCATCTGCTGATGCGCTGCGCGTTTGA 1790
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2396 GCCTTGGCGGCTTAACCTCAGCTCGTCCGCTATGGAACCATCCCGATTTGCCGAA 2455
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 2456 GACTGAGGGCTCTTTCGACACTGCTTTCGATGTGGAACAATGACAAGGA 2503
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Db 1851 CGTGGGGGGCTCCGGGACAGCGTGGCGCGCTTCGACCCCGTTCAACGA 1898
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RESULT 14
US-09-489-039A-3687/c
; Sequence 3687, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3687
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-3687

Query Match 3.2%; Score 83.6; DB 4; Length 1248;
Best Local Similarity 49.2%; Pred. No. 9e-16;
Matches 261; Conservative 0; Mismatches 254; Indels 15; Gaps 1;

QY 1956 CCTCATCTTGGGAATTTCTATGGCAATTTCTCAATGAATTGATCCGGATATATGGATCCG 2015
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Db 582 CATCATGAAGGTGCGGCTGTCCGGAATTTCTCAACGGCGTGTGACGCGGTATCTGGAGCCCG 523
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2016 TACAATGACAACTTTATCCCGGCTCCACTACACTTGTGAGAATGTGTTGAAGGCAAGAGG 2075
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Db 522 CAAACGATCTGCTGCTCGGATGCGCTACGATCGCGACACGCTGAGGAGAGCGGAG 463
QY 2076 GCTGCTAAGAGGCACTGACGACGAGAGTTGGTTACACGAATCGATCTCCCGTCGTA 2135
Db 462 AACACGCGTCAGCTGCAGATTTGCCATGGCCCTGAAGGTCGATGAATAAGCGCGTTGTTT 403
QY 2136 GGAATCGTCACTCGCTGACAGCCCAAAAGGGGATCCACTGATCAAGCATGCGATTAC 2195
Db 402 GCGCTGCTAGCGCTTTTACCAGCCAGAAAGGCTGGACCTGGTGTGAAGCGCTGCCG 343
QY 2196 CGPACACTGAAACGGAACGAGAGTGGTTTGGTTTGGTTTTCAGCGCCGAGCTCGAATC 2255
Db 342 GGTCTGCTTGAAGAGGCGCCAGCTGGCGCTGCTGGCGCGCGGATCCGCTGCTGCAG 283
QY 2256 CAAGCTGATTTGTCAACTGGCGATACGCTCCAGCGGTAACCAATGGCAAGTGAGG 2315
Db 282 GAAGTTTCTTGCCG-----CCGCCCGCGAACAACCCCGGCGCAAGTGGGT 238
QY 2316 CTTTCCTTGACCTACGACGAGCCTCTCTGCACTCTGATATACGCTGGCTCTGACTTCATT 2375
Db 237 GTGCAATTTGGCTACCATGAGGCTTCTCCACCGCATTTATGGCGCGCGCGACGTCATT 178
QY 2376 CTGGTCCCATCTATATTGAGCCTTGGCGGCTTAATCACTGCTGCTGCCATGCGGTATGA 2435
Db 177 CTGGTCCGAGCGCTTTGAACCTCGCGGCTGACCCAGCTGTATGGTCTGAAGTACGGG 118
QY 2436 ACCATCCGATTTGTCGCAAGACTGGAGGCTCTTCGACACTGTCTTCGA 2485
Db 117 AGCTGCGCTGGTGGCGCGACCGCGGCTCTGGCGGACACCGTCTGCTGA 68

RESULT 15

US-09-489-039A-3862
; Sequence 3862, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3862
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3862

Query Match 3.2%; Score 83.6; DB 4; Length 1536;
Best Local Similarity 49.2%; Pred. No. 1e-15;
Matches 261; Conservative 0; Mismatches 254; Indels 15; Gaps 1;
QY 1956 CCTCATCTTTGGGAATTTCTATGTCATTTCTCAATGGAATTTGATCCGGATATATGGATCCG 2015
Db 808 CATCATGAAGTCCGCTGTCGGGAATTTCAACGGGCTTGACGACGGTATCTGGAGCCCG 867
QY 2016 TACATGACAACTTTATCCCGTCCACTACCTTTGTGAGATGTGTTGAAGGCAAGAGG 2075
Db 868 CAAACGATCTGCTGCTGCGGATCGCTAGATCGGCACACGCTGGAGGAGAAGCGGAG 927
QY 2076 GCTGCTAAGAGGSCACTGACGACGAGATTTGGGTTACAGCAATCGATGCTCCCGTCGTA 2135
Db 928 AACACGGTCAGCTGAGATTTGCCATGGGCTGAAGTCTGATGAATAAGCCGTTGTTT 987
QY 2136 GGAATCGTCACTCGCTGACAGCCCAAAAGGGGATCCACTGATCAAGCATGCGATTAC 2195
Db 988 GCGTCTGTCAGCGCTCTTACCAGCCAGAAAGGCTGACCTGGTGTGTTGAAGCGCTGCCG 1047
QY 2196 CGTACACTGAAACGGAACGAGAGTGGTTTTCGTTGTTTTCAGCGCGGACTCTCGAATC 2255

Db 1048 GGTCTGCTTGAACGAGGCGCCAGCTGGCGCTGCTGGCGCGCGGATCCGGTCTGCAG 1107
QY 2256 CAAGCTGATTTTGTCAACCTGGCGAATACGCTTCCAGCGGTAACCAATGGGCAAGTGAGG 2315
Db 1108 GAAGTTTCTTTCGCG-----CCGCCCGCGAACAACCCCGGCGCAAGTGGGT 1152
QY 2316 CTTTCCTTGACCTACGACGAGCCTCTCTGCACTCTGATATACGCTGGCTCTGACTTCATT 2375
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QY 2376 CTGGTCCCATCTATATTGAGCCTTGGCGGCTTAATCACTGCTGCCATGCGGTATGA 2435
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QY 2436 ACCATCCGATTTGTCGCAAGACTGGAGGCTCTTCGACACTGTCTTCGA 2485
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Search completed: June 20, 2004, 12:54:58
Job time : 222 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 05:15:45 ; Search time 1495 Seconds
(without alignments)
7960.983 Million cell updates/sec

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Perfect score: 2598
Sequence: 1 agctgtctgaaataattat.....gtgaacaggcgatctcag 2598

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:
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19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2598	100.0	6027	17	US-10-109-048-1145
3	1204.8	46.4	3693	15	US-10-424-799-1
4	1204.8	46.4	4168	15	US-10-284-668-11
5	931	35.8	2303	15	US-10-284-668-1
6	924.8	35.6	1338	13	US-10-425-114-20351
7	826.4	27.9	2261	13	US-10-425-114-30909
8	724.4	31.8	2518	13	US-10-424-599-97896
9	480.4	18.5	1181	13	US-10-425-114-4321
10	315.8	12.2	585	16	US-10-341-961A-91
11	290.6	11.2	548	9	US-09-739-438-3
12	283.8	10.9	641	13	US-10-424-599-83485
13	207.6	8.0	437	9	US-09-739-438-1
14	186.2	7.2	464	13	US-10-424-599-84418

15 183.8 7.1 297 9 US-09-294-093B-3346 Sequence 3346, Ap
16 176.4 6.8 299 9 US-09-294-093B-3520 Sequence 3520, Ap
17 173 6.7 381 13 US-10-424-599-109987 Sequence 109987,
18 146.6 5.6 2031 13 US-10-425-114-33865 Sequence 33865, A
19 145 5.6 3430 15 US-10-163-214-1 Sequence 1, Appli
20 144.8 5.6 3434 15 US-10-044-543-9 Sequence 9, Appli
21 140.8 5.4 1275 15 US-10-163-214-9 Sequence 9, Appli
22 140.8 5.4 3386 15 US-10-163-214-11 Sequence 11, Appli
23 136.2 5.2 240 9 US-09-294-093B-3300 Sequence 3300, Ap
24 134.4 5.2 3453 15 US-10-163-214-5 Sequence 5, Appli
25 116.4 4.5 1464 16 US-10-369-493-33677 Sequence 33677, A
26 115 4.4 409 13 US-10-424-599-29678 Sequence 29678, A
27 103.8 4.0 1629 13 US-10-424-599-29680 Sequence 29680, A
28 102.6 3.9 1455 16 US-10-369-493-42704 Sequence 42704, A
29 92.4 3.6 965 13 US-10-425-114-14355 Sequence 14355, A
30 90.6 3.5 1419 16 US-10-369-493-33675 Sequence 33675, A
31 90 3.5 1419 16 US-10-369-493-35219 Sequence 35219, A
32 89.2 3.4 1455 16 US-10-369-493-46953 Sequence 46953, A
33 87 3.3 1286 13 US-10-425-114-8641 Sequence 8641, Ap
34 87 3.3 2179 15 US-10-138-075-3 Sequence 3, Appli
35 87 3.3 3290 13 US-10-424-599-64934 Sequence 64934, A
36 85.8 3.3 1383 16 US-10-369-493-44603 Sequence 44603, A
37 85.6 3.3 1440 16 US-10-369-493-35062 Sequence 35062, A
38 85.6 3.3 1440 16 US-10-369-493-38466 Sequence 38466, A
39 85.6 3.3 1440 16 US-10-369-493-38620 Sequence 38620, A
40 85.6 3.3 1440 16 US-10-369-493-38957 Sequence 38957, A
41 85.6 3.3 1502 13 US-10-425-114-31744 Sequence 31744, A
42 85.6 3.3 1828 13 US-10-336-753-48 Sequence 1052, Ap
43 85.6 3.3 2423 13 US-10-336-753-48 Sequence 48, Appli
44 85.6 3.3 2480 17 US-10-109-048-1144 Sequence 1144, Ap
45 85.2 3.3 1419 16 US-10-369-493-38452 Sequence 38452, A

ALIGNMENTS

RESULT 1

US-10-634-262-1
; Sequence 1, Application US/10634262
; Publication No. US20040049810A1
; GENERAL INFORMATION:
; APPLICANT: Myers, Alan M.
; TITLE OF INVENTION: dult Coding for a No. US20040049810A1 Starch Synthase and Uses
; TITLE OF INVENTION: Theroef
; FILE REFERENCE: D6036PCT
; CURRENT APPLICATION NUMBER: US/10/634,262
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US/09/554,467A
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/24225
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/062,102
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 1
; LENGTH: 6027
; TYPE: DNA
; ORGANISM: maize
; FEATURE:
; OTHER INFORMATION: cdna sequence corresponding to the gene encoding the
; OTHER INFORMATION: starch synthase enzyme DUL.
US-10-634-262-1

Query Match 100.0%; Score 2598; DB 13; Length 6027;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCTGAAAAAATTTATTCGCTGGGAAACAGTTGTTTACTTATCCAGATGTTTGA 60

DB 2425 AGCTTCTGAAAAAATTTATTCGCTGGGAAACAGTTGTTTACTTATCCAGATGTTTGA 2484

QY 61 AAGCTGATTCACAAATTTGATCTCTATTTCATTCGATCTATCATGCTGTGGCCAAATGAGC 129

DB 2485 AAGCTGATTCAACAAATTGATCTCTATTTCATTCGATGATCTATCAGCTGTGGCAATGAGC 2544
QY 121 CTGATGTACTTATCAAGAGAGCAATTCATGTGGGTGGAGTGGAGATTTTTCACCTGAAAAAT 180
DB 2545 CTGATGTACTTATCAAGAGAGCAATTCATGTGGGTGGAGTGGAGATTTTTCACCTGAAAAAT 2604
QY 181 TGCACAAAGAGCGAGCTGGCAGGGGACTGTGTGTGTGCAAACTATATACATTTCTTAAGCAGG 240
DB 2605 TGCAACAGAGCGAGCTGGCAGGGGACTGTGTGTGTGCAAACTATATACATTTCTTAAGCAGG 2664
QY 241 CATACAGAAATGACATTTGTGTTTTTAAACGGACACACCGGTATATGAAAAATAATAACAATA 300
DB 2665 CATACAGAAATGACATTTGTGTTTTTAAACGGACACACCGGTATATGAAAAATAATAACAATA 2724
QY 301 ATGATTTCTGTGATACAAATAGAAAGCAACCATGGATGAAAAATTTATTTGAGGATTTCTTGG 360
DB 2725 ATGATTTCTGTGATACAAATAGAAAGCAACCATGGATGAAAAATTTATTTGAGGATTTCTTGG 2784
QY 361 CTGAAGAAAAAGCAACGAGAACTTTAGAACTTTGCAAAATGAGGAAGCTGAAAGGAGGAGAC 420
DB 2785 CTGAAGAAAAAGCAACGAGAACTTTAGAACTTTGCAAAATGAGGAAGCTGAAAGGAGGAGAC 2844
QY 421 AAACCTGATGAGCGCGCGCAATGGAGGAAGAAAGGCGCGCAGATAAAGCTGACAGGGTAC 480
DB 2845 AAACCTGATGAGCAGCGCGCAATGGAGGAAGAAAGGCGCGCAGATAAAGCTGACAGGGTAC 2904
QY 481 AAGCCAAAGTTGAGGTAGAGACGAGAAAGAAATTAATTTGCAATGATTTGGGTTTAGCCA 540
DB 2905 AAGCCAAAGTTGAGGTAGAGACGAGAAAGAAATTAATTTGCAATGATTTGGGTTTAGCCA 2964
QY 541 GAGCTCTCTGTGATTAATTTATGATACATTTGAGCCCATCAGCTGAGCAAGAGGCTACTG 600
DB 2965 GAGCTCTCTGTGATTAATTTATGATACATTTGAGCCCATCAGCTGAGCAAGAGGCTACTG 3024
QY 601 TCAGATGTATTAATACATAAATCAAGACCTTAGTTCACAGTACTGAGATATGGATGC 660
DB 3025 TCAGATGTATTAATACATAAATCAAGACCTTAGTTCACAGTACTGAGATATGGATGC 3084
QY 661 ATGTGGCTTATTAACAAATTCGATTGAGGACTCTCTTTTGTGTAAGGCTTTGTCATCATC 720
DB 3085 ATGTGGCTTATTAACAAATTCGATTGAGGACTCTCTTTTGTGTAAGGCTTTGTCATCATC 3144
QY 721 ATGACAAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 780
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DB 3205 TGGACTGGCTTTTCTGACGCGCCACACGAGGAGTGCAGAGAAATATGACAAATGGAG 3264
QY 841 GACATGATTTTTCATGCTACCTTTCCAAATAACATGACTGAGGAAGAGTATTCGATGGAAG 900
DB 3265 GACATGATTTTTCATGCTACCTTTCCAAATAACATGACTGAGGAAGAGTATTCGATGGAAG 3324
QY 901 AAGAACAAAGGATCTATACAAGCTTTCAACAAGAGAGGAGGAAAGGGAGGAGGCTATTTA 960
DB 3325 AAGAACAAAGGATCTATACAAGCTTTCAACAAGAGAGGAGGAAAGGGAGGAGGCTATTTA 3384
QY 961 AAGGAAGGCTGAGGAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGAGAA 1020
DB 3385 AAGGAAGGCTGAGGAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGAGAA 3444
QY 1021 TGTTCCTGCTTTCTCAGAAACACATTTGTTTACACCGAACCATTTGAAATACATTCCTGGAA 1080
DB 3445 TGTTCCTGCTTTCTCAGAAACACATTTGTTTACACCGAACCATTTGAAATACATTCCTGGAA 3504
QY 1081 CTACTATTGATGTCTTTTAAATCTCTTAAATACAGTTCTAACTGAAAGCCAGAGGTTT 1140
DB 3505 CTACTATTGATGTCTTTTAAATCTCTTAAATACAGTTCTAACTGAAAGCCAGAGGTTT 3564
QY 1141 GGTTCGATGTTCTTTTAAATCTCTTAAATCTCTTAAATCTCTTAAATCTCTTAAATCTCTTAA 1200

DB 3565 GGTTCGATGTTCTTTTAAATCTCTTAAATCTCTTAAATCTCTTAAATCTCTTAAATCTCTTAA 3624
QY 1201 TGGTACAGCAGAGAAATGGTTTCAACCTTAAAGCAACAGTTTACGTTTCAACGAGATGCTT 1260
DB 3625 TGGTACAGCAGAGAAATGGTTTCAACCTTAAAGCAACAGTTTACGTTTCAACGAGATGCTT 3684
QY 1261 ATATGATGGACTTCTGTTTCTCGGAGTCAGAAAGAGGTGGAAATTTATGATAACAGAAATG 1320
DB 3685 ATATGATGGACTTCTGTTTCTCGGAGTCAGAAAGAGGTGGAAATTTATGATAACAGAAATG 3744
QY 1321 GGTTAGACTATCATATCTCTGTTTCTGGTCAATTTGCAAAAGGAAACCATCTATGCAATTTG 1380
DB 3745 GGTTAGACTATCATATCTCTGTTTCTGGTCAATTTGCAAAAGGAAACCATCTATGCAATTTG 3804
QY 1381 TCCACATTTGCTGTGAGATGGCACAATCGCAAGGTTGGAGGCTTCTGGTATGTTGTCA 1440
DB 3805 TCCACATTTGCTGTGAGATGGCACAATCGCAAGGTTGGAGGCTTCTGGTATGTTGTCA 3864
QY 1441 CTAGTCTTTTCACTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATTTCTTCCAAAGT 1500
DB 3865 CTAGTCTTTTCACTGCTGTGCAAGATTTAGGACACAATGTGGAGGTTATTTCTTCCAAAGT 3924
QY 1501 ACGGTTGCTTGAATCTTAAGCAATGTCAAGAAATCTAACAATCCATCAGAGTTTTTCTGGG 1560
DB 3925 ACGGTTGCTTGAATCTTAAGCAATGTCAAGAAATCTAACAATCCATCAGAGTTTTTCTGGG 3984
QY 1561 GTGGTTCTGAATAAATGTGTGGCGTGACGTAGTCGAAGGCTTTGTGTTTACTTTCTCTGG 1620
DB 3985 GTGGTTCTGAATAAATGTGTGGCGTGACGTAGTCGAAGGCTTTGTGTTTACTTTCTCTGG 4044
QY 1621 AACCTCAAAAATGGGATGTTTGGAGTCGGATATGTATATGGCAGGACGATGACCGCCGAT 1680
DB 4045 AACCTCAAAAATGGGATGTTTGGAGTCGGATATGTATATGGCAGGACGATGACCGCCGAT 4104
QY 1681 TTGGTTCTTCTGCTGCTCTGCTCTAGAGTTTCTCTCTCAAAAGTGGATCTTCTCTCGAACA 1740
DB 4105 TTGGTTCTTCTGCTGCTCTGCTCTAGAGTTTCTCTCTCAAAAGTGGATCTTCTCTCGAACA 4164
QY 1741 TAATACATTTGCCATGATTTGGTCAAGTCTCTGTTTGGTCTGCTGCTGCTGCTGCTGCTGCTG 1800
DB 4165 TAATACATTTGCCATGATTTGGTCAAGTCTCTGTTTGGTCTGCTGCTGCTGCTGCTGCTGCTG 4224
QY 1801 CGAAGTCTAGCTTGGCAAAACGACGCGGTGGTATTCACCATCCACAATCTTGAATTTGGAG 1860
DB 4225 CGAAGTCTAGCTTGGCAAAACGACGCGGTGGTATTCACCATCCACAATCTTGAATTTGGAG 4284
QY 1861 CGCATCATTTGGCAAAAGCAATGAGATATTTGTGATAAAGCAACAACTGTCTCTAATACAT 1920
DB 4285 CGCATCATTTGGCAAAAGCAATGAGATATTTGTGATAAAGCAACAACTGTCTCTAATACAT 4344
QY 1921 ATTCAAGAAAGTGTCAAGTCAATGTCATGTCATGTTCTCTCATCTTGGGAAATTTCTATGGCA 1980
DB 4345 ATTCAAGAAAGTGTCAAGTCAATGTCATGTCATGTTCTCTCATCTTGGGAAATTTCTATGGCA 4404
QY 1981 TTCTCAATGGAAATGATCCGGATATATGGGATCCGATACAAATGACAACTTTATCCCGTCC 2040
DB 4405 TTCTCAATGGAAATGATCCGGATATATGGGATCCGATACAAATGACAACTTTATCCCGTCC 4464
QY 2041 ACTACACTTGTGAGATGTTGTTGAGGCAAGAGGCTGCTAAGGGGCACTGCGAGCAGA 2100
DB 4465 ACTACACTTGTGAGATGTTGTTGAGGCAAGAGGCTGCTAAGGGGCACTGCGAGCAGA 4524
QY 2101 AGTTTGGGTTACAGCAAAATCGATGTCCTCGCTGTAGGAATCGTCTCACTCGCTGACAGCCC 2160
DB 4525 AGTTTGGGTTACAGCAAAATCGATGTCCTCGCTGTAGGAATCGTCTCACTCGCTGACAGCCC 4584
QY 2161 AAAAGGGATCCACTGATCAAGCATGCGATTTACCGTACACTCGAAGCGAACGAGCAGG 2220
DB 4585 AAAAGGGATCCACTGATCAAGCATGCGATTTACCGTACACTCGAAGCGAACGAGCAGG 4644
QY 2221 TGGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 2280
DB 4645 TGGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 4704

2281 ATACGCTCCACGGCGTAAACCATGGCGAAGTGAGGCTTTCCTTGAACCTACGACGAGCCTC 2340
4705 ATACGCTCCACGGCGTAAACCATGGCGAAGTGAGGCTTTCCTTGAACCTACGACGAGCCTC 4764
2341 TCTCGCATCTGATATAGCTGGCTCTGACCTTCACTCTGGTCCCATCTATATTTTGGCCTT 2400
4765 TCTCGCATCTGATATAGCTGGCTCTGACCTTCACTCTGGTCCCATCTATATTTTGGCCTT 4824
2401 CGGCGCTTAACTCAGCTCGTCCCATGGCTGATGGAACCATCCCGATTTGTCGCAAGACTG 2460
4825 CGGCGCTTAACTCAGCTCGTCCCATGGCTGATGGAACCATCCCGATTTGTCGCAAGACTG 4884
2461 GAGGCTCTTTCGACACTGTCTTGATGTGACATGACAAAGGACCGGCGGAGATCGAG 2520
4885 GAGGCTCTTTCGACACTGTCTTGATGTGACATGACAAAGGACCGGCGGAGATCGAG 4944
2521 GCCTTGAGCCCAACGGGTTTAGCTTTGACGAGGCTGATGACAAAGGATTTGACTACGCGC 2580
4945 GCCTTGAGCCCAACGGGTTTAGCTTTGACGAGGCTGATGACAAAGGATTTGACTACGCGC 5004
2581 TGAACAGGCGATCTCAG 2598
5005 TGAACAGGCGATCTCAG 5022

RESULT 2
US-10-109-048-1145
; Sequence 1145, Application US/10109048
; Publication No. US20040107461A1
; GENERAL INFORMATION:
; APPLICANT: COMMURI, PADMA
; APPLICANT: KBELING, PETER L.
; APPLICANT: RAMIREZ, NORA
; APPLICANT: MCKEAN, ANGELA
; APPLICANT: GAO, ZHONG
; APPLICANT: GUAN, HANPING
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS
; FILE REFERENCE: 2461-76
; CURRENT APPLICATION NUMBER: US/10/109,048
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/279,720
; PRIOR FILING DATE: 04/01-03-10
; NUMBER OF SEQ ID NOS: 1154
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1145
; LENGTH: 6027
; TYPE: DNA
; ORGANISM: Zea mays
US-10-109-048-1145

Query Match 100.0%; Score 2598; DB 17; Length 6027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGCTTCTGTAAGAAAATATTTCCTGGGAAACAAAGTTGTTTACTTATCCAGATGTATTGA 60
2425 AGCTTCTGTAAGAAAATATTTCCTGGGAAACAAAGTTGTTTACTTATCCAGATGTATTGA 2484

61 AAGCTGATTCACAAATGATCTCTATTTCATTCGTGATCTATCAGCTGTGGCCAAATGAGC 120
2485 AAGCTGATTCACAAATGATCTCTATTTCATTCGTGATCTATCAGCTGTGGCCAAATGAGC 2544

121 CTGATGATCTTATCAAGAGGATTCATTAATGGTGGAAAGTGAGATTTTCACTGAAAAAT 180
2545 CTGATGATCTTATCAAGAGGATTCATTAATGGTGGAAAGTGAGATTTTCACTGAAAAAT 2604

181 TGCACAGAGGAGCTGGCGGGGACTGGTGGTCTGCAACTATACATTCCTAAGCAGG 240
2605 TGCACAGAGGAGCTGGCGGGGACTGGTGGTCTGCAACTATACATTCCTAAGCAGG 2664

241 CATACAGATGGACTTTGTGTTTTTAAACGGACACACGAGTATATGAAAAATAAACAATA 300

2665 CATACAGATGGACTTTGTGTTTTTAAACGGACACACGGTATATGAAAAATAAACAATA 2724
301 ATGATTTCTGTGATACAAATAGAAAGCACCATGATGAAAAATTTATTTGAGGATTTCTTGG 360
2725 ATGATTTCTGTGATACAAATAGAAAGCACCATGATGAAAAATTTATTTGAGGATTTCTTGG 2784
361 CTGAAAAAGCAACAGAGAACTTGAGAACTTTCGCAATAGAGGAGCTGAAAGAGGAGAC 420
2785 CTGAAAAAGCAACAGAGAACTTGAGAACTTTCGCAATAGAGGAGCTGAAAGAGGAGAC 2844
421 AAATCATGATGAGCAGCGCGAAATGAGAGAAAGGCGCGAGATAAGCTTGACAGGCTAC 480
2845 AAATCATGATGAGCAGCGCGAAATGAGAGAAAGGCGCGAGATAAGCTTGACAGGCTAC 2904
481 AAGCCAAAGGTTGAGGTTAGAGACGAAAGAAATAAATTTGTCAATGTATTGGGTTTAGCCA 540
2905 AAGCCAAAGGTTGAGGTTAGAGACGAAAGAAATAAATTTGTCAATGTATTGGGTTTAGCCA 2964
541 GAGCTCCTGTTGATATATTTATGATATTGATGAGCCCATCAGACTGGAACAAGAGCTACTG 600
2965 GAGCTCCTGTTGATATATTTATGATATTGATGAGCCCATCAGACTGGAACAAGAGCTACTG 3024
601 TCAGATTTGATTAATAACATAAACTCAAGACCTCTAGTTTACAGTACTGAGATATGATGC 660
3025 TCAGATTTGATTAATAACATAAACTCAAGACCTCTAGTTTACAGTACTGAGATATGATGC 3084
661 ATGGTGGCTATATAACAAATGGATTTGATGAGCTCTCTTTTGTGTAAGGCTTTTTCATCATC 720
3085 ATGGTGGCTATATAACAAATGGATTTGATGAGCTCTCTTTTGTGTAAGGCTTTTTCATCATC 3144
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3145 ATGACAAAGATTTGATTTGATGAGCTTTTGCAGATGTTTCTGCTGCTGAAAGACATATGTAT 3204
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3205 TGGACTGGGTTTTTGTGCTGACGGCCACCAAGGAGTGCAGGAATTTATGACAAATGGAG 3264
841 GACATGATTTTCATGCTACCCCTTCCAAATTAACATGACTGAGGAAGAGTATTGGATGGAAG 900
3265 GACATGATTTTCATGCTACCCCTTCCAAATTAACATGACTGAGGAAGAGTATTGGATGGAAG 3324
901 AAGAACAAAGGATCTATACAGGCTTTCACACAGAGGAGGAGGAGGAGGAGGCTATTTA 960
3325 AAGAACAAAGGATCTATACAGGCTTTCACACAGAGGAGGAGGAGGAGGAGGCTATTTA 3384
961 AAGAGGAGGCTGAGAGAAATGCAAAAATGAAAGCTGAGATGAAAGGAAAGACCTATGAGAA 1020
3385 AAGAGGAGGCTGAGAGAAATGCAAAAATGAAAGCTGAGATGAAAGGAAAGACCTATGAGAA 3444
1021 TGTTCTCTGTTTCTCAGAAACACATTTGTTTACACCGAACCATTTGAAATACATGCTGGAA 1080
3445 TGTTCTCTGTTTCTCAGAAACACATTTGTTTACACCGAACCATTTGAAATACATGCTGGAA 3504
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3505 CTACTATTCATGCTGCTTATATTCCTTCTAATAACAGTTCTTAACTGGAAGCCAGAGGTTT 3564
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3625 TGTTTCAAGCAGAAATGTTTTCACCTTAAAGCAACAGTTTACGTTTCCACGAGATGCCT 3684
1261 ATATGATGACTTCTGTTTCTCGAGTCAAGAGAGTGGAAATTTATGATAACAGAAATG 1320
3685 ATATGATGACTTCTGTTTCTCGAGTCAAGAGAGTGGAAATTTATGATAACAGAAATG 3744
1321 GGTTAGACTATCATATTCCTGTTTGGGTCAATTCGAAAGGAAACCCCTTATGCAATTTG 1380
3745 GGTTAGACTATCATATTCCTGTTTGGGTCAATTCGAAAGGAAACCCCTTATGCAATTTG 3804

1449 AGCAAGAGAGAGGCTGCAAGAAAAGAAAGATTTGCGAGAAATGATGCTAAAGCCAC 1508
542 AGCTCCTGTTGATAATTTATGGTACATTTAGGCCCATCAAGACTGGACAAGAGGCTACTGT 601
1509 GAAGACTCGTGATATCACGCTGGTACATAGAGCCAAAGTGAATTTAAATGCGAGGACAAGGT 1568
602 CAGATTGTAATTAACAATAAATCAAGACCTCTAGTTTACAGTACTCAGATATGGATGCA 661
1569 CAGTTATATCTATAACAAGATTCAGTCTCTCTCCATGCTAAGACCTTGTGGATCCA 1628
662 TGTGGCTATAACAATTTGATTTGATGACTCTCTTTTGTCTGAAAGGCTTGTTCATCATCA 721
1629 CGGAGGATATAATTTGGAAGATGTTGTCTATTGTCAAAAGCTTGTAAATCTGA 1688
722 TGAACAAGATTTGATTTGGTGGTTGAGATGTTGTGCTGCTCCCTGAAAGAACATATGTAAT 781
1689 GAGATAGATGGTGAATTTGGTGGTATACAGAGGTTGTTATTCTCTGATCAGGCACCTTTCTT 1748
782 GGACTGGTTTTTGTGACGGCCCAAGAGGAGTGAAGGAATTTATGACAAACATGGAGG 841
1749 GGATTTGGTTTTTGTGATGGTCCACCAAGCATGCCATTTGCTTTATGATAACAACTACCG 1808
842 ACATGATTTTCATGCTACCTTCCAAATAACATGACTGAGGAAGATTTGATGGAAGA 901
1809 CCAAGACTTCCATGCTATTTGCCCAACCAATTCGGAGGAATTAATTTGGGTTGAGGA 1868
902 AGAACAAGATCTATACAGGCTTCAACAAGAGAGGAGGAAGGAGGAGGCTATTAA 961
1869 AGAACAATCAGATCTTTAAGACCTTTCAGGAGGAGAGAGGCTTAGAAGCGGCTATGG 1928
962 AAGCAAGGCTGAGAGAAATCAAAAATGAAGCTGAGATCAAGGAAAGACTATGAGAA 1021
1929 TGCTAAGTTGAAAAACAGACACTTCTGAAAACTGAAACAAAGAAAGAACTATGAATC 1988
1022 GTTCTCGTTTCTCAGAAAACACATGTTTACACCGAACCACTTGAATAATCATGCTGAAC 1081
1989 ATTTTACTGCTCAGAAAGCATGATGATATATCTGAGCCTCTTGATATCAAGCTGAAG 2048
1082 TACTATTGATGCTTTATTAATCTTCTAATACAGTTTCACTAAGTGAAGGAGGTTTG 1141
2049 CAGCGTCACAGTTTACTATTAATCCGCCAATACAGTACTTTAATGGTAAACCTGAAATTTG 2108
1142 GTTTCGATGTTCTTAAATGTTGGATGATACAGGTGGGGTGTGCCACTCAGAAAGAT 1201
2109 GTTCAGATGTTCAATTAATCGCTGACTCACGGCTGGGTCATTCGCACTCAGAAAT 2168
1202 GGTACAGCAGAAAATGGTTCAACCTTAAAGCAACAGTTTACGTTCCACGAGATGCCA 1261
2169 GTCCGCTGCTGAAAATGGCAACCATGTGACAGCAACTGTGAAGGTTCCATTGGATGCATA 2228
1262 TATGATGACTCTGTTTTCTCGGAGTCAGAGAGGTTGGAATTTATCATACAGAAATGG 1321
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1322 GTTAGACTATCATATTCCTGTTTGGGTCAATTTGCAAGGAACCACTATGACATTTG 1381
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1382 CCACATTTGCTGTTGAGATGGCACCAATTCGCAAGGTTGGAGGCTTGGTGAATGTCAC 1441
2349 CCATATTGCTGTCGAAATGGCAACCAATGCAAGGTTGGAGGCTTGGTGAATGTCAC 2408
1442 TAGTCTTTACGCTGCTGCAAGATTTAGGACCAATGTGAGGATTTATCTTCCAAAGTA 1501
2409 TAGTCTTTCCGCTGCTTCAAGATTTAAACCATAATGTGGATTAATCTTACTTAAGTA 2468
1502 CGGTGCTTGAATCTAAGCAATGTCAAGAAATCTACAAATCCATCAGAGTTTCTTGGGG 1561
2469 TGACTGTTTGAAGATGAATATGTGAAGGACTTTCGGTTTCAAAAACACTTTTGGGG 2528
1562 TGGTTCTGAATAAATGTGTGGGCTGACCTAGTCGAAAGGCTTTGTGTTTACTTCTGGA 1621

2529 TGGGACTGAATAAAGATATGTTGTTGAAAAGGTGGAAGGTCTCTCGTCTATTATTTTGGGA 2588
1622 ACCTCAAAATGGAGTGTGTTGGAGTCGGATATGATATG---GCAGGACGATGACCGCG 1678
2589 GCCTCAAAAACGGGTATTTTCGAAAAGGGTGGCTCTATGGTTGTAGCAATGATGGTGAACG 2648
1679 ATTTGGCTTCTTCTGTCGTTCTGCTCTAGAGTTTCTCCCTCCAAAGTGGATCTTCTCCGAA 1738
2649 ATTTGGTTTCTTCTGTCACGGGCTTTGGAGTTTCTTCTGCAAGGTGGATTTAGTCGGA 2708
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2709 TATCATTTCAATGTCATGATTTGGTCTAGTCTCTGTTGCTTGGCTCTTTTAAAGGAACAATA 2768
1799 CGGGAAGTCTAGTTGGCAACCGCACGGTGGTATTTCACATCCACAATCTTGAATTTGG 1858
2769 TACACATATGTTCTAAGCAAAATCTGTTATGTTCTTACGATACATAATCTTGAATTTGG 2828
1859 AGGCAATCATATTTGGCAAGCAATGAGATTTGTGATAAGCAACAACTGCTCTTAATAC 1918
2829 GGCAATCTCATTTGGGAGGCAATGACTAACGCAACAAAGCTTACACAGTTTCAACAAC 2888
1919 ATATTCAAGGAAGTCTCAGGTCATGGTGCATAGTTCCTCATCTTGGGAAATTTCTATGG 1978
2889 TTACTCACAGGAGTGTCTGGAACCCCTGTAATTTGGGCTTCACTTCAACAAGTTCCATGG 2948
1979 CATTTCTCAATGGAATTTGATCCGGATATATGGGATCCGTACATGACAACCTTTATCCGGT 2038
2949 TATAGTGAATGGGATTTGACCCAGATATTTGGGATCTCTTTAAACGATAAGTTCAATCCGAT 3008
2039 CCACTACACTTGTGAGATTTGTTGAAGCAAGAGGCTGTCTAAGAGGCACTGCAGCA 2098
3009 TCCGTACACTCAGAAAACGTTGTTGAAGGCAAAAACAGCAGCCAAAGAGCTTTGACGG 3068
2099 GAAGTTTGGTTACAGAAAATCGATGTCCCGCTGCTAGGAAATCGTCACTCGCCTGACGC 2158
3069 AAAAATTTGACTGAAAACAGGCTGACCTTCTTTGGTAGGAATTTATCACCCTTAACTCA 3128
2159 CCAAAAAGGAGTCCACTGATCAAGCATCGATTCACCTGATACACTGMAAGGACGAGCA 2218
3129 CCAGAAAGGAATCCACTCAATTAACATGCTATTTGGCGCACCTTGGAAACGGAACGAGCA 3188
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3189 GGTAGTCTTGTGTTTCTGCTCTGATCCTAGGGTACAAAACGATTTGTAAATTTGGC 3248
2279 GAATACTCCACGGGCTAAACCAATGGGCAAGTGAAGCTTTCCTTGAACCTTACGACGAGCC 2338
3249 AAATCAATTTGCACTCCAAAATATAATGACCGCGCACGACTCTGTCTAACATATGACGAGCC 3308
2339 TCTCTCGCATCTGATATAGCTGGCTCTGACTTTCATTTCTGTTGCCATCTATATTTTGGCC 2398
3309 ACTTTCTCACCTGATATATGCTGGTCTGATTTTATTTCTAGTTTCTTCAATATTTGAGCC 3368
2399 TTCCGCCCTAACTCAGCTCGTCCCATGGGATGGAACCAATCCGATTTGTCCGCAAGAC 2458
3369 ATGTGACTTAACACAACCTTACCGCTATGAGATGTTCAATTTCCAGTCTGTGGTAAAC 3428
2459 TGAAGGCTCTTCGACACTGTCTTTCGATGGAACATGACAAGGAACGAGCCCGAGATCG 2518
3429 TGAAGGACTTTATGATATCTGTTTATGTTGATGTTGACCATGACAAAGAGAGAGCAACAGTG 3488
2519 AGSCCTTGAGCCCAACGGGTTTAGCTTTCAGCGAGCTGATAGCAACGGTGTGACTACGC 2578
3489 TGTGCTTGAACCAAAATGGGATTCAGCTTTGATGAGCAGATGCTGGCGGAGTTGATTTATGC 3548
2579 GCTGAACAGGGGATCTCAG 2598
3549 TCTGATAGAGCTCTCTCTG 3568

RESULT 4

US-10-284-668-11

/ Sequence 11, Application US/10284668
/ Publication No. US20030106100A1
/ GENERAL INFORMATION:
/ APPLICANT: Kossmann, Jens
/ Abel, Gernot
/ TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMS
/ INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
/ PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FISH & NEAVE
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10020
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/284,668
/ FILING DATE: 29-Oct-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/836,567
/ FILING DATE: 24-JUL-1997
/ APPLICATION NUMBER: PCT/EP95/04415
/ FILING DATE: 09-NOV-1995
/ APPLICATION NUMBER: DE P 44 41 408.0
/ FILING DATE: 10-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haley Jr., James F.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: Agrevo-4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-596-9000
/ TELEFAX: 212-596-9090
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4168 base pairs
/ TYPE: nucleotide
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to RNA
/ ORIGINAL SOURCE:
/ ORGANISM: Solanum tuberosum
/ STRAIN: cv. Desire
/ TISSUE TYPE: leaf tissue
/ IMMEDIATE SOURCE:
/ LIBRARY: cDNA-library in Lambda ZAPII
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 307..3897
/ SEQUENCE DESCRIPTION: SEQ ID NO: 11:
/ US-10-284-668-11

Query Match 46.4%; Score 1204.8; DB 15; Length 4168;

Best Local Similarity 66.7%; Pred. No. 0;

Matches 1735; Conservative 0; Mismatches 862; Indels 3; Gaps 1;

QY 2 GCTTGTGAAAAAATTATTCGTCGGGAAACAGTTCTTTACTTATCCAGATGATGAA 61

Db 1176 GCTTGGCGAGAAAAATTATGAAGGGATCAGATATTTTGTTCAGAGGTTGTAAA 1235

QY 62 AGCTGATTCACAAATTGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCCAATGAGCC 121

Db 1236 ACCTGATGAGAGCTCGAGATATTTCTTAACAGAGGTCITTTCCACITTTGAAGATGAGTC 1295

QY 122 TGATGTAATCAAGAGAGCATTCATGAGGTTGAGTGGAGATTTTCTACTGAAAAATT 181

Db 1235

Db 1296 TGATGCTTGTATTATGGGAGCTTTTATATGATGGCGCTATAGTCTTTTACTACAAGGCT 1355
QY 182 GCACAAGAGCGAGCTGGCAGGGGACTGGTGGTCTGCGAAACTATATACATTCCTTAACAGGC 241
Db 1356 AACTGAGACTCATCTCAATGGAGATTGGTGGTCTTTCAGAGATCCCATGTGTTCCCAAGAAAC 1415
QY 242 ATACAGAAATGACTTTGTGTTTTTAAACGACACACCGGTATATGAAAAATAATAACAATAA 301
Db 1416 ATACAGGCTGATTTTGTGTTTTTAAATGGACAAGATGCTATGACAACAATGATGGAAA 1475
QY 302 TGATTTCTGTATACAAATAGAAAGCACCATGGATGAAAATTTTATTTGAGGATTTCTTGCC 361
Db 1476 TGACTTCAGTATAACTGTGCAAGGTGGTATGCAAAATCATTTGACTTTGAAAAATTTCTTGT 1535
QY 362 TGAAGAAAAGCAACGAGAACTTTGAAACCTTCCAAATGAGGAGCTGAAAGAGGAGACA 421
Db 1536 TGAGGAGAAATGGAGAGAACAGGAGAAACTTGTCTAAAGAACCAAGCTGAAAGAGAAAGACT 1595
QY 422 AACTGATGAGCAGCGCGCAATTCGAGAGAAAGAGCGCGCAGATAAAAGCTGACAGGCTACA 481
Db 1596 AGCGGAGAGAACAAAGACGATAGAGAGCAGAGAAAGCTGAAATTTGAGCTGACAGAGACA 1655
QY 482 AGCCAAAGGTTGAGGTAGAGACGAAAGAAAGATAAATTTGCAATGTAATTTGGGTTTACCCAG 541
Db 1656 AGCAAAAGGAAAGAGGCTGCAAAAGAAAAGAAAGTATTTGCGAGAAATTCATGTTAAAGCCAC 1715
QY 542 AGCTCCTGTTGATAATTTATGTTGATACATTTGAGGCCCATCAGACTGCGAAGAGGCTACTGT 601
Db 1716 GAAGACTCGTGATATCACGTGGTACATAGAGCAAGTGAATTTAAATGCGGAGACAAGGT 1775
QY 602 CAGATTGATTAACATAAACTCAAGACCTCTAGTTCACAGTACTGACATATGATGATCA 661
Db 1776 CAGGTTATATAACAAAAGTTCAAGTCTCTCTCCCATGCTAAGGACTTGTGGATCCA 1835
QY 662 TGTGTGCTATAACAATTTGATGAGTGGACTCTCTTTTGTGCTGAAAGCTTTGTTTCATCATCA 721
Db 1836 CGGAGGATATAAATTTGGAAGGATGTTGTCTATTTGTCAAAAAGCTTTGTTAAATCTCA 1895
QY 722 TGACAAGATTTGTGATTTGGTGGTTTGCAGATGTTCTCGTGCCCTGAAAGAACATATGATT 781
Db 1896 GAGAATAGATGTTGATTTGGTGGTATACAGAGGTTGTTATTCCTGATCAGGCACTTTCTT 1955
QY 782 GGACTGGGTTTTTGTCTGACGGCCCAAGGAGTCAAGGAATTTATGACAAACAATGGAG 841
Db 1956 GGATTTGGGTTTTTGTCTGATGTTCCACCCCAAGCATGCCATTTGTTATGATAACATCACCG 2015
QY 842 ACATGATTTTCTGTTACCCCTTCCAAATAACATGACTGAGGAGAGATTTGATGTAAGA 901
Db 2016 CCAAGACTTCCATGCCATTTGTCCCAACCAACATTCGCGAGGAATTTATTTGGGTTGAGGA 2075
QY 902 AGAACAAAGGATCTATACAAGGCTTCAACAAGAGAGGAGGAAAGGAGGAGCTATTAA 961
Db 2076 AGAACATCAGATCTTTAAGACACTTCAGAGGAGAGAAAGCTTTAGAGAAGCGGCTATGCG 2135
QY 962 AAGGAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAAAGGAAAGAAAGCTATGAGAA 1021
Db 2136 TGCTAAGGTTGAAAAAACAAGCACTTCTGAAAACCTGAAACAAAGGAAAGAACTATGAAATC 2195
QY 1022 GTTCTCGGTTTCTCAGAAAACAATTTGTTTACHACCGAACCACTTGAAATACATCTCTGGAAC 1081
Db 2196 AITTTTACTGTCTCAGAAAGCATGTAGTATATATCTGAGCCCTCTTGATATCAAGAGCTGGA 2255
QY 1082 TACTATTTGATGCTTTTATAATCTTCTAATACAGTTCCTAATCTGAAAGCCAGAGGTTTG 1141
Db 2256 CAGGCTCAGATTACTATATCCCGCCCAATACAGTACTTAATGTPAAACCTGAAATTTG 2315
QY 1142 GTTTCGATGTTCTTTTAAATCGTTGGATGATATCACGTTGGGGTGTTCGCCACCTCAGAAGAT 1201
Db 2316 GTTCAGATGTTCTTTTAAATCGTGGACTCACCGCCCTGGGTCCCATTTGCCACCTCAGAAAT 2375
QY 1202 GGTACAGAGAGAAATGTTTACACCTTAAAGCAACAGTTTACGTTCCAGAGATGSCCTA 1261
Db 2376 GTCGCCTCTGAAAAATGGCAACCATGTCTAGAGCAACTGTGGAAGGTTCCATTTGATGATCA 2435

ORGANISM: Solanum tuberosum
STRAIN: cv Berolina
TISSUE TYPE: tuber tissue
IMMEDIATE SOURCE:
LIBRARY: cdna-library in pBluescript-SKII+
FEATURE:
NAME/KEY: CDS
LOCATION: 3..2033
OTHER INFORMATION: /function= "Polymerization of starch"
/product= "Starch synthase"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-284-668-1

Query Match 35.8%; Score 931; DB 15; Length 2303;
Best Local Similarity 68.5%; Pred. No. 1.1e-268;
Matches 1301; Conservative 0; Mismatches 595; Indels 3; Gaps 1;
QY 703 AAAGGCTTGTTCATCATCATGACAAAGATGTGATGTGGTTGCGATGTTGTCGTGC 762
DB 13 AAAGGCTTGTTCATCATCATGACAAAGATGTGATGTGGTTGCGATGTTGTCGTGC 72
QY 763 CTGAAGAGACATATGATTTGGACTGGGTTTTCGTGACGGCCACCAGGAGTGCAGGA 822
DB 73 CTGATCAGGCATTTCTTCTGGATTTGGGTTTTCGTGATGTTCCACCCAAAGCATGCCATTG 132
QY 823 ATTATGACAAACATGAGGACATGATTTTCATGCTACCCCTTCCAAATAACATGACTGAGG 882
DB 133 CTATGATAACAATCACCCCAAGACTTCCATGCCATTGTCCTCCCAACCATTCGGAGG 192
QY 883 AAGAGTATTTGGATGGAAGAGAACAAAGATCTATCAAGGCTTCAACAGGAGAGAGG 942
DB 193 AATATTATTTGGTTGAGGAGAACATCATGATCTTTAAGACACTTCAGGAGAGAGAGGC 252
QY 943 AAAGGAGGAGGACTATTAAGAGAGGCTGAGAGAAATGCAAAATGAAAGCTGAGATGA 1002
DB 253 TTAGAGAGCGGCTATGCGTGAAGGTTGAAAGAACAGCATCTTGGAAATCTGAAACAA 312
QY 1003 AGGAAAGACTATGAGATGTTCTCGTTTCTCAGAAAACACATTTGTTTACCGCAACAC 1062
DB 313 AGGAAAGACTATGAAATCATTTTACTGTCACAGAGCATGTATATATATCTGAGCCTC 372
QY 1063 TTGAATATCATGCTGGAACCTATATTTGATGTGCTTTTATATCTTCTTCTTCTTCTTCT 1122
DB 373 TTGATATCAAGCTGGAAGCAGCTCACAGTTTACTATTAATCCCGCAATACAGTACTTA 432
QY 1123 CTGGAAGCCAGAGGTTTGGTTTGCATGTTCTTTTAACTCGTTGGATGTATCCAGTGGGG 1182
DB 433 ATGTTAACTGAAATTTGGTTTCAATGTTTCAATTTTATCGTGGACTCACCGCTGGGTC 492
QY 1183 TGTTCACCTCAGAGATGGTACAGCAGAAAATGGTTTCAACCTTAAAGCAACAGTTT 1242
DB 493 CATTTGCACCTCAGAAAATGTCGCTGCTGAAAATGGCACCCATGTTCAGAGCAACTGTGA 552
QY 1243 AGTTTCCAGCAGATGCCTATATATGAGACTTCTGTTTCTCGAGATCAGAAAGGTGGAA 1302
DB 553 AGGTTCCATTTGATGCATATATGATGATTTTGTATTTTCCGAGAGAGAGATGTTGGGA 612
QY 1303 TTTATGATAACGAATGGTTAGACTATCATATCTCGTTTTCGTTTTCGTTTTCGTTTTCG 1362
DB 613 TTTTGTGACAAAGAGCGGAATGGACTATCATACCTGTGTTTGGAGGATCGCTTAAAG 672
QY 1363 AACCACTATGACATGTCCTCATTTGCTGTTTGGATGCGCAACCAATCGCAAGGTTGGAG 1422
DB 673 AACCTCCAATGATATTTGCTCATATTTGCTGCAATGGCAACCAATGGCAAGGTTGGAG 732
QY 1423 GTCTGGTATGTTGTCATGCTCTTTCAGTGTGCTGTGCAAGATTTAGGACAAATGTGG 1482
DB 733 GCTTGGTATGTTGTTTACTAGTCTTTCCTCGTGTCTCAAGATTTAAACCAATATGTGG 792
QY 1483 AGGTTATTTCTCCAAAGTACGGTTGCTGAATCTAAGCAATCTCAAGATCTACAAATCC 1542
DB 793 ATATATCTTACCTAAGTATGACTGTGTTGAAGATGAATAATGTGAAGGACTTTTCGGTTTC 852

QY 1543 ATCAGAGTTTCTTCTGGGTTGTTCTGAAATAAATGTGTGGGCTGGAAGTCTGAGAGCC 1602
DB 853 ACAGAACTACTTTTGGGTTGGGACTGAAATYAAAAGTATGGTTTGGAAAGTGGAGGTC 912
QY 1603 TTTGTGTTTACTTCTCGAACCTCAAAATGGGATGTTTGGAGTCGGATATGATATG--- 1659
DB 913 TCTCGGTTCTATTTTGGAGCCTCAAAAGGGTTATTTTCGAAAGGGTGGTCTATGGTT 972
QY 1660 GGAGGACGATGACCGCGATTTGGCTTCTTCTGTGCTTCTCTCTAGAGTTTCTCTCC 1719
DB 973 GTAGCAATGATGGTGAACGATTTGGTTCTTCTGTCAAGCGGCTTTTGAGATTTCTTCTGC 1032
QY 1720 AAAGTGGATCTTCTCCGAACATAATACATATGCAATGTCATGATTTGGTCAAGTCTCTCTGTGCT 1779
DB 1033 AAGTGGATTTAGTCCGATATCAITCAITGTCATGTTGGTCTAGTGTCTCTGTGTCT 1092
QY 1780 GGTACACAAGGAAACTACGCGAAGTCTAGCTTGGCAAAACGACGGTGTATTCACCA 1839
DB 1093 GGCTCTTTAAGGAACAATATACACACTATGTTCTAAGCAATCTCGTATAGTCTTACGA 1152
QY 1840 TCCACATCTTGAATTTGGAGCGCATCATATTTGGCAAAAGCAATGAGATTTGTGATAAG 1899
DB 1153 TACATAATCTTGAATTTGGGCGAGATCTCATTTGGAGAGCAATGACTAACGACAGAAAG 1212
QY 1900 CAAACAATGTTCTTAATATACATATTCAAAAGGAGTCTCAGGTCAATGTCCTCTCTCT 1959
DB 1213 CTAGAACAGTTTCCCAACTTACTCAGAGGAGTGTCTGGAAAACCTGTATTTGGGCTC 1272
QY 1960 ATCTTTGGGAAATTTATGGCAATTTCTCAATGGAATTTGATCCGGATATATGGGATCCGTACA 2019
DB 1273 ACCTTTCACAGTTTCCATGTTAGTGAATGGATTGACCCAGATATTTGGGATCTCTTAA 1332
QY 2020 ATGACAACTTTATCCCGTCTCACTACATTTGTGAGATTTGTTGAAGGCAAGAGGCTG 2079
DB 1333 AGATAAGTTTCAATCCGATTCGGTACACTCAGTCAAAAGCTTTGTTGAAGGCAAAACAGCAG 1392
QY 2080 CTAGAGGCGCTGCGAGCAGAAAGTTTGGTTTACAGCAATCGATCTCCCGCTGCTGAGAA 2139
DB 1393 CCAGGAAGCTTTGCGAGGAAACCTTGAATGAAACAGGCTGACCTTCTTTGGTAGGAA 1452
QY 2140 TGTCTCACTCGCTGACAGCCCAAGAGGAGTCCACCTGATCAAGCATGCGATTTCAACGTA 2199
DB 1453 TTATCACCGGTTTAACTCACAGAAAGAAATCCACCTCATTTAAACATGCTATTTGGGCA 1512
QY 2200 CACTCGAAGGAAACGAGCAGGTGTTTGTGTTGTTTCAAGCGCGGACTCTCGAATCCAG 2259
DB 1513 CTTTGGAAACGGAACGGAAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1572
QY 2260 CTGATTTTGTCAACCTGCGCAATACGCTTCCAGCGGCTAAACCATGGGCAAGTGAAGGCTTT 2319
DB 1573 ACGATTTTGTAAATTTGGCAATCAATTTGCACTCCAAATATTAAGCCGCGACGACTCT 1632
QY 2320 CTTGACCTACGAGAGCTCTCTGGCATCTGATATACGCTGGCTCTGACTTCAATTCGG 2379
DB 1633 GTCTAACATATGAGAGCCACTTTCTCACCTGATATATGCTGTGTTGTTTATTTCTAG 1692
QY 2380 TCCCATCTATATTTGAGCCTTTCGCGCTTAACTCAGCTCGTCCCATGCGGTATGGAACCA 2439
DB 1693 TTTCTTCAATATTTGAGCCATGTGAGCTTAAACAACTTACCGCTATGAGATATGTTTCAA 1752
QY 2440 TCCGATTTGTCGCAAGACTGAGGCTTCTTCGACACTGTTCTCGATGTGACAAATGACA 2499
DB 1753 TTCCAGTCTGCTGTAABACTTGAAGGACTTTATGATCTGATTTGATTTGATGTTGACATGACA 1812
QY 2500 AGGAACGAGCCGAGATGAGGCTTTGAGCCAAACGGGTTTGTAGCTTTTACGCGAGCTGATA 2559
DB 1813 AAGAGAGAGCAACAGGTGTGTTCTTGAACCAATGGAATTCAGCTTTGATGAGCAGATG 1872
QY 2560 GCAAGGTTGTTGACTACGCGCTGAACGGGCGATCTCAG 2598
DB 1873 CTGCGGAGGTTGATTTATGCTCTGATAGAGCTCTCTCTG 1911

1140 TGGTTTCAGATGTCCTTTAAATCGTTGGATGATCCAGTGGGGTGTGGCCACCTCAGAAG 1199
1141 |||||
362 TGGTTTCAGAGGTTCTTTTAAACGGTTGGACTCATCCAGTGGTCCCTTACCACACAGAAG 421
1200 ATGGTACAGCAGAGAAATGGTTTACACCTCAAAAAGCAACAGTTTACGTTTCCACGAGATGCC 1259
422 ATGGTAAAGGCTGAGAATGGTTTACACCTTACGAACAAACAG---GGTTCCCTTGGATGCA 477
1260 TATATGATGAGCTTCGTTTTCGAGAGTCAGAGAGTGGAAATTTATGATAACAGAAAT 1319
478 TATATGATGAGCTTCGTTTTCGAGAGTCAGAGAGTGGAAATTTATGATAACAGAAAT 534
1320 GGGTTAGACTATCATATTCCTGTTTGGGTCAAATTCGAAAGGAACCACTTATGCACATT 1379
535 GGGATGGAATCATATTCCTGTTCTGATCTGATCTGTTGCAAGGGAACCTTCCAAATGATATT 594
1380 GTCCACATTCGTTTGAATGGCAACCAATTCGAAAGGTTGAGGTCCTTGGTGAATTTGTC 1439
595 GTACACATTCGAGTGGAAATGGTCTCTATCGCAAGGTCGGAGGCTTTGGTGAATTTGTT 654
1440 ACTAGTCTTTACGTCGTCGCAAGATTTAGACACAAATGTTGGAGGTTATTTCTCCAAAG 1499
655 ACAAGCCTTTTACGAGCTGTTCAAGATTTAGGCCATTAAGTTGAGGTTATTTCTGCCGAAA 714
1500 TACGGTTGCTTCAATCTAAGCA----- 1521
715 TATGATTTGTTAAACCTTAAACAGTGAAGTTTGTCTACTGGTGTAAATGTCTCGGTCT 774
1522 ----- 1521
775 TCTTTTCTTCCCTTTTATCTGTCTCTCCTCACTTTCTTTCAATTTCCAAATTT 834
1522 ----- 1521
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1550 TTTTCTTGGGGTGGTTCTGAAATAAATGTGGCGTGGACTAGTCGAAGGCTTTTGTGT 1609
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1910 CTCTAATACATATTTCAAGGAAGTGTGAGTCTCAGTCTATGGTGCATAGTTCTCTCATCTTGGAA 1969
1435 ATCCGATACATCTCGAAGGAAGTGGCGGACATGGAGCTATTTCACCTCACTACTATAA 1494
1970 ATTCTATGGCAATTTCTAATGGAATTTGATCCGGATATATGATGGATCCGTACATGACACTT 2029
1495 ATTCCATGGAATTTGAAATGGAATTTGATCTCTGATATTTGGATTCATATATGACAAAT 1554
2030 TATCCCGGTCCACTACACTTTGTGAAATGTGGTTGAAGGCAAGAGGCTGCTAAAGAGGC 2089
1555 TATTCGGGTCAATTTATCATCAGAAATTTGTTGAGGCGCAGAGTGTCTGCAAAAAGGC 1614
2090 ACTCAGCAGAGTTCGGGTTTACGCAAAATCGATGTCCCCGTCTGTAGAAATTCGTCATCG 2149
1615 ATTCCAGCAGATCTTGGATTTACAGCAAACTGATACCCCTGTTTGTGAAATCATCACTCG 1674
2150 CCTGACAGCCCAAAAGGGGATCCACCTGATCAACAGATCGGATTCACCGTACACTCGAACG 2209
1675 TCTAACAGTTTCAAGAGGGAATCCACCTTATCAAAACATGCAATGTCATCGAGCTCTTGAACG 1734
2210 GAAAGGACAGTGTGTTTGTGTTTTCAGCGCCGGAATCTCGAATCCAAAGCTGATTTTGT 2269
1735 CAATGGACAGTGTGTTTCTGAGGTTCTGACAGATCTTCCGATACAAAGTGAATTTAC 1794
2270 CAACCTGCGCAATACGCTCCACGGCTGAACCAATCGGCAAGTGGAGCTTTCTTTGACCTA 2329
1795 AAATTTGCGCAATGAGTGTGATGAAATCAATGCGCGAGTGAAGCTATGCTCTAAACCTA 1854
2330 CGAGAGCTCTCTCGCATCTGATATACGCTGGCTCTGACTTCAATCTCTGCTCCATCTAT 2389
1855 TGACGAGCACTGTCAATTTGATATATGCTGGCGAGACTTCATTCGTTCTCTCCAT 1914
2390 ATTTGAGCTTTCCGCTTAACTCAGCTCGTCCCATGGGTATGGAACCACTCCGATTTGT 2449
1915 CTTGAACTTTGTTGTTTAAACAGCTTATTTGCTATGGCTATGGATCCATCCAGTTGT 1974
2450 CCGCAAGACTCGAGGCTCTTTTCGACACTGTCTTGGATGGAACAATGACAAGGAACGAGC 2509
1975 TCGGAAACTCGAGGCTGTACGACACCGTTTGTGATGTCGACATGATAAGGATCGGGC 2034
2510 CCGAGATCGAGGCTTTGAGCCCAACGGGTTTAGCTTTGACGGAGCTGATAGCAACGGTGT 2569
2035 TCAAGCAAGGCTCTCGAGCCAAATGGATTCAGTTTGAAGAGCTGATAGCAAGTGTGT 2094
2570 TGACTACGCTGTGAACAGGCGAT 2593
2095 GGATTTATGCTCTCGACAGGCAAT 2118

RESULT 8

US-10-424-599-97896
; Sequence 97896, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 97896
; LENGTH: 2218
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59413C.1
US-10-424-599-97896

Query Match

27.9%; Score 724.4; DB 13; Length 2218;

Db 301 TGTGGAATCATCTCTGCTTAACAGGTTCAGAGGGAATCCACCTTATCAAAACATGCAAT 360
Qy 2192 TCACGCTACACTCGAAACGGAACGAGAGTGGTTTGTCTTGTCTCAGCGCGGACTCTCG 2251
Db 361 GCATCGAGCTCTTGNACCAATGAGAGTGGTTTACTCTGGGTTCTGCACAGATCTCTG 420
Qy 2252 AATCAAGCTGATTTGTCAACCTGGGGAATACGCTCCACGGGTAAACCATGGGCAAGT 2311
Db 421 CATACAAAGTGACTTTTACAAATTTGGCCAGTAAGCTGCATGCTGTAATACCATGGCCAGT 480
Qy 2312 GAGGCTTCTTGTACCTACGAGGAGCTCTCTCGATCTGATATACGCTGCTGACTT 2371
Db 481 GAAGCTATGTCTAACCTATGACGAGCCACTGTCAATTTGATATATATGCTGGCGAGCTT 540
Qy 2372 CATCTGCTCCCATCTATATTTGAGCCTTGGGCTTAACCTCAGCTCGTCGCCATGCGGTA 2431
Db 541 CATCTCTGCTCTCCATCTTCGAACCTTGTGCTCAACACAGCTTATTTGCTATGCGCTA 600
Qy 2432 TGAACCAATCCGATGTTCCGCAAGACTGGAGGGCTCTTCGACACTGCTTCGATGTGA 2491
Db 601 TGAATCCATCCAGTGTTCGGAATCTGGAGGCTGTACGACCCGTTTGTGATGTGCA 660
Qy 2492 CAATCAGAGGAACGAGCGGAGATCGAGGCTTCGAGCCCAACGGTTTAGCTTTGACGG 2551
Db 661 CAATGATAGGATCGGCTCAAGCAAGGTCTCGAGCCAAATGGATTCAGTTTCGAAGG 720
Qy 2552 AGCTGATAGCAACGGTGTGTGACTACGCGCTGAACAGGGCGAT 2593
Db 721 AGCTGATAGCAAGTGTGTGATGATGCTCTCGACAGAGCCAT 762

RESULT 10

US-10-341-961A-91
; Sequence 91, Application US/10341961A
; Publication No. US20040006787A1
; GENERAL INFORMATION:
; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
; APPLICANT: Curagen Corporation
; APPLICANT: Craata, Oswald
; APPLICANT: Swirsky, Peter
; APPLICANT: Mysore, Kixan
; APPLICANT: Folkerts, Otto
; APPLICANT: Martin, Gregory
; APPLICANT: Ekengren, Sophia
; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGEN
; FILE REFERENCE: BTI. 67A2
; CURRENT APPLICATION NUMBER: US/10/341,961A
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: 60390249
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60261029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60348792
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 91
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-341-961A-91

Query Match 12.2%; Score 315.8; DB 16; Length 585;
Best Local Similarity 71.4%; Pred. No. 9.4e-84;
Matches 416; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

Qy 1030 TTCTCAGAACACATGTTTACACGGAACCACTTGAATACATGCTGGAACTACTATTG 1089
Db 3 TGTCTCAGAGCATGTAGTATATATCTGAGCCTCTTGATATCCAACTGGAAGCAGCTCA 62
Qy 1090 ATGTGCTTTATATCTCTTAATACAGTTTCTAACTGGAAGGCCAGAGGTTTGTGTTTCGAT 1149

Db 63 CAGTTTACTAATATCCCGCCAAATACAGTACTTAAATGTAAACCTGAAATTTGGTTCAAT 122
Qy 1150 GTTCCTTTAATCGTTGATGTATCCAGGTGGGTTGTTGCCACCTCAGAAATGTTCAAG 1209
Db 123 GTTCATTTAATGCTGACACACCGCTGGTCCATTGCCACCTCAGAAATGTTGCTG 182
Qy 1210 CAGAAATGTTTACACCTTAAGACACAGTTTACGTTTCCACGAGATGCCCTATATGATGG 1269
Db 183 CTGAAATGGCACCCATGTCAAAGCAACTGTCAAGGTTCCATTGGATGCATATATGATGG 242
Qy 1270 ACTTCGTTTCTCGAGCTCAGAAAGGTGGAATTTATGATAACAGAAATGGGTTAGACT 1329
Db 243 ATTTGTATTTTCCGAGAGAGAGATGGTGTATTTTGGCAATAGCGGATGACT 302
Qy 1330 ATCATATCTCTGTTTGGGTCAATGCAAGGAACCACTATGCAATGTCACATTTGCCATTTG 1389
Db 303 ATCATATACCGTGTGTTGGAGGAGTCGCTAAAGAACCTCCGATGCATATTTGCCATATTG 362
Qy 1390 CTGTTGAGATGGCACCAATCGCAAGGTTCGAGCTCTTGGTGTATTTGCTACTAGTCTTT 1449
Db 363 CTGTGCAAAATGGCACCAATTCGAAAGGTGGAGGCTTGGTGTATTTGTTACTAGCCTTT 422
Qy 1450 CACGTGCTGTGCAAGATTTAGGACACAAATGTGGAGGTTATTTCTTCCAAAGTACGGTTGCT 1509
Db 423 CCGTGTCTGTTCAAGATTTAAACCAATATGTGGACATTTATCTTACCTAAGTATGACTTT 482
Qy 1510 TGAATCTAAGCAATGTCAAGATCTCAAAATCCATCAGAGTTTTCTTGGGTTGGTTCTG 1569
Db 483 TGAAGATGAATAATGTGAAGGACTTTCGGTTTCAAAAAGCTACTTTTGGGTTGGGACTG 542
Qy 1570 AATAAATGTGCGGTGGGACTAGTCGAAGGCCCTTTGTGTTTA 1612
Db 543 AATAAAGTATGTTTGGAAAGGTGGAGGACTCTCGGTCTA 585

RESULT 11

US-09-739-438-3
; Sequence 3, Application US/09739438
; Patent No. US20020029394A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Thorpe, Cathy
; TITLE OF INVENTION: Homologs of Starch Synthase D1
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/739,438
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/171514
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (312)
; NAME/KEY: unsure
; LOCATION: (408)
; NAME/KEY: unsure
; LOCATION: (548)
US-09-739-438-3

Query Match 11.2%; Score 290.6; DB 9; Length 548;
Best Local Similarity 79.9%; Pred. No. 3.5e-76;
Matches 341; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1661 GAGGACGATGACCCGCAATTTGGCTTCTTCTGCTGTTCTGCTAGAGTTTCTCTCA 1720
Db 3 CAGCAATGACGAGATAGATTTGGCTTCTTCTGCAATTTCTGCTAGAGTTTCTCCGCA 62

Db 122 TAAAGCTTTGTTTAACTATGATGAGCGCACTATCTCAATTGATTGCTGGTCCGACT 181
Qy 2371 TCATTCTGGTCCCATCATATATTGAGCCTTTCGGCCCTCACTCAGCTCGTCCCATCGGT 2430
Db 182 TCATCCTTGTTCCTTCCATGTTTGAACCTTGTGTTTAACTCCAGCTTACTGCTATCGTT 241
Qy 2431 ATGGAACATCCCGATTGTCGCGAAGACTGAGGGCTCTTCGACACTGCTTCGATGCG 2490
Db 242 ATGGATCTATCCCAATAGTTTCGAAAACCTGAGGCCCTTATGACACCGTTTTCGACGTCG 301
Qy 2491 ACAATGACAAAGGACGAGCCGAGATCGAGCCCTTGAGCCCAACGGGTTTAGCTT-TGAC 2549
Db 302 ACGATGATGAGATCGAGCTCGACACAGGCTTTCGACCAACGGGTTCAATTCGAA 361
Qy 2550 GGAGCTGATGACAA-CGGTGTGACTAGCGCTGAAACAGGGCGATCTC 2596
Db 362 GGAGCTGACANCAACGGGTGTGGATTACCCCTTTCACAAAGGATCAC 409

RESULT 14
US-10-424-599-84418
; Sequence 84418, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kowalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 84418
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MPT3847_47245C.1
US-10-424-599-84418

Query Match 7.2%; Score 186.2; DB 13; Length 464;
Best Local Similarity 62.6%; Pred. No. 9e-45;
Matches 290; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

Qy 300 AATGATTTTGGTATCAAAATAGAAAGCAACCATGATGAAATTTATTGAGATTTCTTG 359
Db 2 AAAGACTTCTGCATACCCGTTTGATGGAGGATGGATGCAATTAGCATTTTGAAGATTTCTTG 61
Qy 360 GCTGAGAAAGCAACGAGAACTTGAGAACCTTGCAATGAGGAGCTGAAAGGAGGAGA 419
Db 62 CTTGAGGAGAAACGTPAAAGAAATTGAAAGAACTTGTCTGGGCCAAGCTGAAAGGGAAGA 121
Qy 420 CAAACTGATGACAGCGGCGAATGAGGAGAAAGAGGCGGCGAGATAAAGCTGACAGGGTA 479
Db 122 CAACTGAGAGCAAGGCGAATGAGGAGAGAGAGAGCTGCAAGAGAGAGAGAGGCA 181
Qy 480 CAAAGCAAGGTTGAGGTAGAGACGAGAGAGAAATAAATTGTGCAATGTATTTGGTTTAGCC 539
Db 182 CGGGCGAAGGCGGAGGTTGGAAGATGCGAGAAACATTTGCCACAATTTGTGAAAAATGCT 241
Qy 540 AGAGCTCCTGTTGATAATTTATGTTACATTTAGGCCCATCACGCTGGACAGAGGCTACT 599
Db 242 GTAAAGTCCATTGATAATGTTTGGTATATTGAACTTAGTAATCAAGGCGCAATGAAATTG 301
Qy 600 GTCAGATTGATTATAACATAAATCAAGACCTCTAGTTTCACAGTACTGAGATATGATG 659
Db 302 ATCAGATTATATTAAACAGAGCTCAGTCTCTTGTGCAATGCTAATGAATATGGATT 361
Qy 660 CATGTTGGCTATAACAAATTTGATGAGTCTCTTTTGTGAAAGGCTTTTCAATCAT 719
Db 362 CATGGGGGGCACAATAATTTGGAAGTAGTATTATCAATCGTTGAAAGGCTTGTCAAGTCT 421

Qy 720 CATGACAAAGATTGTGATTTGGTGGTTTGCAGATGTTTGTGCTGC 762
Db 422 GTTCTAAAAGAGGTGAATGGTGGTATGCTGATGTTGTTGTAC 464

RESULT 15

US-09-294-093B-3346
; Sequence 3346, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Ialugudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 3346
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700379870H1
; NAME/KEY: unsure
; LOCATION: 2, 56, 78, 121, 125, 155, 187-188, 197, 270
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-3346

Query Match 7.1%; Score 183.8; DB 9; Length 297;
Best Local Similarity 77.1%; Pred. No. 3.3e-44;
Matches 229; Conservative 0; Mismatches 67; Indels 1; Gaps 1;

Qy 1832 ATTCACCATCCCAATCTTGNATTTGGCGCATCATATTGGCAAGCAATGAGATATTG 1891
Db 1 ANTACCATCCCAATCTTGGATTTGGAGCGCATCACATTTGGCAAGGCAATGGCANATTG 60
Qy 1892 TGATAAAGCAACAACCTGTCTCTAATACATATTTCAAAGGAAGTGTCAAGTCAATGGTCCAT 1951
Db 61 TGACAAAGCTACACTGNATCCGATACATCTCGAAGAACTGGCCGACATGGAGCTAT 120
Qy 1952 AGTTCCTCATTTGGGAAAATTTCTATGGCATTTCTCAATGGAAATTCGCGATATATGGGA 2011
Db 121 NGCANTCCTACTATATAAATTCATGGAATTCGANATGGAATTTGATCCTGATATTTGGGA 180
Qy 2012 TCCGTACAAATGACAACTTTATCCCGTCCACTACACTGTGTGAGAAATGTGTTGAAGGCAA 2071
Db 181 TCCATANNCTGACAAANTTATTCGGTCCATATATACATCAGAGAAATGTGTTGAGGGCAA 240
Qy 2072 GAGGCGTCTTAAGAGGCGACTGACAGCAAGT-TTGGTTTACAGCAAAATCGATGCC 2127
Db 241 GAGTGTGCAAAAAGGCAATTCGACAGAGANTTACTGGATGACACAAACTGATACCC 297

Search completed: June 20, 2004, 13:20:02
Job time : 1501 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 05:01:30 ; Search time 9811 Seconds
(without alignments)
7907.649 Million cell updates/sec

Title: US-10-634-262-1_COPY_2425_5022

Perfect score: 2598

Sequence: 1 agtctgctgaaaaattat.....gtgacaggcgatctcag 2598

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_esthc:*

9: gb_esttl:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_estfun:*

15: em_estom:*

16: em_gss_hum:*

17: em_gss_inv:*

18: em_gss_pln:*

19: em_gss_vrt:*

20: em_gss_fun:*

21: em_gss_mam:*

22: em_gss_mus:*

23: em_gss_pro:*

24: em_gss_rtd:*

25: em_gss_pbg:*

26: em_gss_vrl:*

27: gb_gss1:*

28: gb_gss2:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2468.2	95.0	6030	11	AY110586 Zea mays
2	771.4	29.7	971	14	CD437215
3	746.4	28.7	773	14	CA404552
4	731.6	28.2	751	14	CD445384

5	683.6	26.3	705	14	CD442124
6	577.6	26.1	692	14	CD434207
7	523.8	20.2	579	14	CA195121
c	519.8	20.0	535	14	CF051954
9	517.4	19.9	571	14	CD433067
c	517.4	19.9	831	12	BG319783
c	488.4	18.8	1014	14	CK247929
c	470.5	18.1	638	28	BZ970127
c	463.6	17.8	1042	14	CK207070
c	461.8	17.8	791	14	CD436069
c	459	17.6	466	14	CF038283
15	456.6	17.6	610	9	AW065975
16	456.2	17.6	695	14	CA498218
17	446.4	17.2	1024	14	CK206780
18	439.4	16.9	662	28	BZ970123
19	438.8	16.9	646	13	BU970315
c	436.4	16.8	782	10	AW448009
c	436.4	16.8	782	13	BQ605700
23	434.6	16.7	651	9	AV835062
24	431.4	16.6	441	14	CF647322
25	424.6	16.3	709	12	BG416819
26	418.8	16.1	804	11	AY110971
27	416.6	16.0	882	12	BI406367
28	414.2	15.9	602	12	BI075226
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c	398.8	15.4	627	14	CD974691
31	389.4	15.0	805	14	CF436116
32	378.4	14.6	827	14	CA764813
c	376	14.5	822	29	CG195829
34	375.2	14.4	556	13	BU970246
35	373.6	14.4	560	13	BU972071
36	369.4	14.2	627	12	BJ478159
37	363	14.0	548	13	CA096498
38	360.4	13.9	536	14	CD891997
39	359	13.8	680	12	BG591409
40	354.2	13.6	687	14	CA840457
41	352.4	13.6	613	14	CF588535
42	347	13.4	690	14	CF436584
43	340.8	13.1	545	12	BJ271418
44	326.8	12.6	555	9	AU101290
45	326.6	12.6	531	14	CD425532

ALIGNMENTS

RESULT 1	AY110586	AY110586	Zea mays	CL1800_1	mRNA	linear	HTC	17-OCT-2002
LOCUS	DEFINITION	Zea mays	6030 bp					
ACCESSION	AY110586							
VERSION	AY110586.1	GI:21214995						
KEYWORDS	HTC							
SOURCE	Zea mays							
ORGANISM	Zea mays							
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.							
AUTHORS	Hayney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.							
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes							
JOURNAL	Unpublished (2002)							
REFERENCE	2 (bases 1 to 6030)							
AUTHORS	Co, E.H.							
TITLE	Direct Submission							
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA							

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES
source Location/Qualifiers

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/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 95.0%; Score 2468.2; DB 11; Length 6030;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 1 AGCTTGCTGAAAAAATATTCCTGCGGAAACAAAGTTGTTTATCTTATCCAGATGTAATGA 60
DB 2425 AGCTTGCTGNNNNNNNTATTTCGCTGGGAAACAAAGTTGTTTATCTTATCCAGATGTAATGA 2484

QY 61 AAGCTGATTCACAAATGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCCAATGAGC 120
DB 2485 AAGCTGATTCACAAATGATCTCTATTTCAATCGTGATCTATCAGCTGTGGCCCAATGAGC 2544

QY 121 CTGATGTACTTATCAAGGAGCAATCAATCGGTGGAGTGGAGATTTTCACTGAAAAAT 180
DB 2545 CTGATGTACTTATCAAGGAGCAATCAATCGGTGGAGTGGAGATTTTCACTGAAAAAT 2604

QY 181 TGCACAGAGCGAGCTGGCAGGAGCTGGTGGTCTGCAAACTATACATTCCTAAGCAGG 240
DB 2605 TGCACAGAGCGAGCTGGCAGGAGCTGGTGGTCTGCAAACTATACATTCCTAAGCAGG 2664

QY 241 CATACAGAAATGGATTTGTGTTTTTAAACGACACACCGGTATATGAAATAATAACAATA 300
DB 2665 CATACAGAAATGGATTTGTGNNNNNNAAACGACACACNNNNNNNNNNNNNNNNNN 2724

QY 301 ATGATTTTCGTGATACAAATAGAAAGCCATGGATGAAATTTATTTGAGGATTTCTTGG 360
DB 2725 NNNNNNNCGTGATACAAATAGAAAGCCATGGATGAAATTTATTTGAGGATTTCTTGG 2784

QY 361 CTGAGAAAGACACGAGAACTTCAGAACCTTGCAAAATGAGAAAGCTGAAAGGAGGAGAC 420
DB 2785 CTGAGAAAGACACGAGAACTTCAGAACCTTGCAAAATGAGAAAGCTGAAAGGAGGAGAC 2844

QY 421 AAACTGATGAGCAGCGGCGATGAGGAGAAAGGCGCGCAGATAAAGCTGACAGGCTAC 480
DB 2845 AAACTGATGAGCAGCGGCGATGAGGAGAAAGGCGCGCAGATAAAGCTGACAGGCTAC 2904

QY 481 AAGCCAGGTTGAGGTAGAGACGAGAAAGATAAATTTGTGCAATGTATTTGGTTAGCCA 540
DB 2905 AAGCCAGGTTGAGGTAGAGACGAGAAAGATAAATTTGTGCAATGTATTTGGTTAGCCA 2964

QY 541 GAGCTCCGTTGATATTTATTTGTTGATCTGAGCCCATCAGCTGGACAGAGGCTACTG 600
DB 2965 GAGCTCCGTTGATATTTATTTGTTGATCTGAGCCCATCAGCTGGACAGAGGCTACTG 3024

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DB 3025 TCAGATTTGATATTAACATAAATCAAGACCTCTAGTTTCAAGTACTGAGATATGGATGC 3084

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DB 3085 ATGTGGCTATAA CAATTTGATTTGATGACACTCTTTTGGTGAAGGCTTCTCATCATC 3144

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DB 3145 ATGACAAAGATTTGATTTGGTGGTTTGCAGATGTTGTCTGCTGAAAGAACATATGTAT 3204

QY 781 TGGACTGGGTTTCTGCTGACCGGCCACACGAGGAGTGCAGAAATTTATGACAAATGGAG 840

DB 3205 TGGACTGGGNNNNNNCTGACGGGCCACACGAGGAGTGCAGAAATTTATGACAAATGGAG 3264

QY 841 GACATGATTTTCATGCTACCCCTTCCAAATATACATGACATGAGGAGATTTTGGATGGAG 900

DB 3265 GACATGATTTTCATGCTACCCCTTCCAAATATACATGACATGAGGAGATTTTGGATGGAG 3324

QY 901 AAGAAACAAAGGATCTATACAAAGGCTTCAACAGAGAGGAGGAGGAGGAGGCTATTA 960

DB 3325 AAGAAACAAAGGATCTATACAAAGGCTNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3384

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DB 3385 AAGGAGGCTGAGAGAAATGCAAAAATGAAAGCTGAGATGAGGAGAAAGACTATGAGAA 3444

QY 1021 TGTTCCTGGTTCTCAGAAACACATTTGTTTACACGAAACCATTTGAAATACATGCTGAA 1080

DB 3445 TGTTCCTGGTTCTCAGAAACACATTTGTTTACACGAAACCATTTGAAATACATGCTGAA 3504

QY 1081 CTACTATTGATGCTGCTTTTATAATCCTTCTAATACAGTTCTAACTGSAAGCCAGAGTTT 1140

DB 3505 CTACTATTGATGCTGCTTTTATAATCCTTCTAATACAGTTCTAACTGSAAGCCAGAGTTT 3564

QY 1141 GGTTCGATGTTTCTTTAATCGTTGGATGTATCCAGGTGGGTGTTGCCACCTCAGAA 1200

DB 3565 GGTTCGATGTTTCTTTAATCGTTGGATGTATCCAGGTGGGTGTTGCCACCTCAGAA 3624

QY 1201 TGTGTAACAGCAAGAAATGGTTTACACCTAAAGCAACAGTTTACGTTTCCACGAGATGCT 1260

DB 3625 TGTGTAACAGCAAGAAATGGTTTACACCTAAAGCAACAGTTTACGTTTCCACGAGATGCT 3684

QY 1261 ATATGATGACATTCGTTTCTCGGAGTCAGAGAGAGTGGAAATTTATGATAACAGAAATG 1320

DB 3685 ATATGATGACATTCGTTTCTCGGAGTCAGAGAGAGTGGAAATTTATGATAACAGAAATG 3744

QY 1321 GGTTAGCATATCATATTCCTGTTTTTGGTCAATTCGAAAGAACACCTATGACATTCG 1380

DB 3745 GGTTAGCATATCATATTCCTGNNNNNGGTTCAATTCGAAAGAACACCTATGACATTCG 3804

QY 1381 TCCACATTTGCTGTTGAGATGGCACCAATCGAAAGCTTGGAGCTTGTGTTGATGTTGTC 1440

DB 3805 TCCACATTTGCTGTTGAGATGGCACCAATCGAAAGCTTGGAGCTTGTGTTGATGTTGTC 3864

QY 1441 CTAGTCTTTTCAGCTGCTGTGCAAGATTTAGGACACAATGTGAGAGGTTATTTCTTCCAAGT 1500

DB 3865 CTAGTCTTTTCAGCTGCTGTGCAAGATTTAGGACACAATGTGAGAGGTTATTTCTTCCAAGT 3924

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DB 3925 ACGTTGCTTTGATCTTAAGCAATGTCAAGAACTCTCAAAATCCATCAGAGTTTTTCTTGG 3984

QY 1561 GTGGTTCTGAAATAAATGTTGGTGGTGGATAGTCTGCAAGGCTTTGTGTTTACTTCTGG 1620

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DB 4045 AACCTCAAAATGGGATGTTGGAGTCGGATATGTATATGCGAGGAGCGATGACCGCGAT 4104

QY 1681 TTGGCTTTCTTCTGCTGTTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAACA 1740

DB 4105 TTGGCTTTCTTCTGCTGTTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCCGAACA 4164

QY 1741 TAATACATTCGCAATGCTCAAGTCTCTGTTGCTGGCTACACAGGAAATACG 1800

DB 4165 TAATACATTCGCAATGCTCAAGTCTCTGTTGCTGGCTACACAGGAAATACG 4224

QY 1801 CGAAGTCTAGCTTGGCAAAACGACGGGTGGTATTTCAACATCCCAATCTTGAATTTGGAG 1860

DB 4225 CGAAGTCTAGCTTGGCAAAACGACGGGTGGTATTTCAACATCCCAATCTTGAATTTGGAG 4284


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QY 2598 G 2598
Db 785 G 785

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LOCUS ELO1N0519H05.g Endosperm_4 Zea mays cdna, mRNA sequence.
DEFINITION CA404552
ACCESSION CA404552.1 GI:24769423
VERSION EST.
KEYWORDS
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 773)
Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
Sequencing of the maize endosperm ESTs
Unpublished (2002)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
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Location/Qualifiers
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XhoI"

ORIGIN
Query Match 28.7%; Score 746.4; DB 14; Length 773;
Best Local Similarity 93.2%; Pred. No. 3.2e-183;
Matches 750; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 18 CGGATATGATATGGCAGGACGATGACCGCGGATTTGGCTTCTTCTGCTGCTGCTCT 77

QY 1706 AGAGTTTCTCTCCAAAGTGGATCTTCCGAAACATATACATGCCATGATGGTCAAG 1765
Db 78 AGAGTTTCTCTCCAAAGTGGATCTTCTCCATACATATACATGCCATGATGGTCAAG 137

QY 1766 TGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1825
Db 138 TGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 197

QY 1826 GGTGGTATTCACCAATCTTGAATTTGGAGCGCATATATGGCAAGCAATGAG 1885
Db 198 GGTGGTATTCACCAATCTTGAATTTGGAGCGCATATATGGCAAGCAATGAG 257

QY 1886 ATATTGTGATAAAGCAACATGCTCTCTAATAATATTAATCAAGGAAGTGTGAGTCAATGG 1945
Db 258 ATATTGTGATAAAGCAACATGCTCTCTAATAATATTAATCAAGGAAGTGTGAGTCAATGG 317

QY 1946 TGCCATAGTCTCTATCTTGGGAATCTATGGCAATCTCAATGAATGATCCGGATAT 2005
Db 318 TGCCATAGTCTCTATCTTGGGAATCTATGGCAATCTCAATGAATGATCCGGATAT 377

QY 2006 ATGGGATCCGATGACATCTTATCCCGTCCACATACCTCTGTGAGATGCTGTTGA 2065
Db 1561 ATGGGATCCGATGACATCTTATCCCGTCCACATACCTCTGTGAGATGCTGTTGA 1620

378 ATGGATCCGTACATGACAACTTTATCCCGGTCCACTACACTTGTGAGAAATGTTGTA 437
2066 AGCAAGAGGGCTGCTAAGAGGGGCACTGACAGAGATTTGGTTTACAGCAATCGATGT 2125
438 AGCAAGAGGGCTGCTAAGAGGGGCACTGACAGAGATTTGGTTTACAGCAATCGATGT 497
2126 CCCGTCGTAGGATCGTCACTCGGCTGACAGCCCAAAAGGGGATCCACCTGATCAAGCA 2185
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2186 TCGGATTCACCGTCACTCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 2245
558 TCGGATTCACCGTCACTCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 617
2246 CTCTCGATTCAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 2305
618 CTCTCGATTCAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 677
2306 GCAAGTGGAGGCTTCTTGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 2365
678 GCAAGTGGAGGCTTCTTGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 737
2366 TGACTTCATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2401
738 TGACTTCATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 773

RESULT 4
CD445384 751 bp mRNA linear EST 03-JUN-2003
LOCUS ELO1N0450H08.b Endosperm_4 Zea mays cdna, mRNA sequence.
DEFINITION CD445384
ACCESSION CD445384.1 GI:31361027
VERSION EST.
KEYWORDS
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 751)
Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
Sequencing of the maize endosperm ESTs
Unpublished (2002)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
Location/Qualifiers
1..751
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm 4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

FEATURES
source
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/mol_type="mRNA"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm 4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 28.2%; Score 731.6; DB 14; Length 751;
Best Local Similarity 98.8%; Pred. No. 2.3e-179;
Matches 737; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1501 ACAGTTCTTCAATCAAGCAATCTCAAGATCTCAAGATCTCAAGATCTCAAGATCT 1560
Db 6 AGGTTCTTCAATCAAGCAATCTCAAGATCTCAAGATCTCAAGATCTCAAGATCT 65

QY 1561 GTGGTTCTCAATAAATATGTTGGGCTGAGTAGTCGAAGGCTTGTGTTTCTCTCTGG 1620
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ORGANISM	Zea mays		605	ATTGTATTATAACATAAACTCAAGACCTCTAGTTCCAGTACTGAGATATGATGATGATG	564
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		601	ATGTATTATAACATAAACTCAAGACCTCTAGTTCCAGTACTGAGATATGATGATGATG	660
AUTHORS	Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and Messing, J.		665	TGCTATTAACAAATGGATTGATGGACTCTCTT	696
TITLE	Sequencing of the maize endosperm ESTs		661	TGCTATTAACAAATGGATTGATGGACTCTCTT	692
JOURNAL	Unpublished (2002)		RESULT 7	CA195121	
COMMENT	Contact: Lai, Jinsheng Dr. Joachim Messing's lab Waksman Institute, Rutgers University 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801 Fax: 732-445-5735 Email: jlai@waksman.rutgers.edu Seq primer: T3.		LOCUS	CA195121	
DEFINITION			DEFINITION	SCAGSB1089G09.g SB1 Saccharum officinarum cDNA clone SCAGSB1089G09	
ACCESSION			ACCESSION	CA195121	
VERSION			VERSION	CA195121.1	GI:35223049
KEYWORDS			KEYWORDS	EST.	
SOURCE			SOURCE	Saccharum officinarum	
ORGANISM			ORGANISM	Saccharum officinarum	
REFERENCE			REFERENCE	Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.	
AUTHORS			AUTHORS	The libraries that made SUCEST	
TITLE			TITLE	Genet. Mol. Biol. 24 (1-4), 1-7 (2001)	
JOURNAL			JOURNAL	Contact: Arruda, P.	
COMMENT			COMMENT	Centro de Biologia Molecular e Engenharia Genetica	
FEATURES			FEATURES	Universidade Estadual de Campinas	
source			source	Caixa Postal 6010, 13083-970, Campinas SP, Brazil	
Query Match	26.1%; Score 677.6; DB 14; Length 692;		Query Match	20.2%; Score 523.8; DB 14; Length 579;	
Best Local Similarity	98.7%; Pred. No. 2.7e-165;		Best Local Similarity	95.2%; Pred. No. 3.3e-125;	
Matches 693; Conservative	0; Mismatches 9; Indels 0; Gaps 0;		Matches 551; Conservative	0; Mismatches 27; Indels 1; Gaps 1;	
Qy	5	TGCTGAAAAAATATTCGCTGGGAACAGTGTGTTACTATCCAGATGATTGAAAGC 64	Qy	833	CAATGGAGGACATGATTTTCATGCTACCTTCCAAATAACATGACCTGAGGAGGATTTG 892
Db	1	TGCTGAAAAAATATTCGCTGGGAACAGTGTGTTACTATCCAGATGATTGAAAGC 60	Db	1	CAATGGAGGACATGATTTTCATGCTACCTTCCAAATAACATGACCTGAGGAGGATTTG 60
Qy	65	TGATTCACAAATGATCTCTATTTCATCTGATCTATCAGCTGTGCCAATGAGCTGA 124	Qy	893	GATGGAAGAAGACAAAGGATCTATACAGCTTCAACAGAGAGGAGGAGGAGGAGGA 952
Db	61	TGATTCACAAATGATCTCTATTTCATCTGATCTATCAGCTGTGCCAATGAGCTGA 120	Db	61	GATGGAAGAAGACAAAGGATCTATACAGCTTCAACAGAGAGGAGGAGGAGGAGGA 120
Qy	125	TGTACTTATCAAGGAGCATTCAATGGGTGGAGTGAGATTTTCTACTGAAAAATGCA 184	Qy	953	GGCTATTAAAGGAGGAGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAGGAGGAG 180
Db	121	TGTACTTATCAAGGAGCATTCAATGGGTGGAGTGAGATTTTCTACTGAAAAATGCA 180	Db	121	GGCTATTAAAGGAGGAGCTGAGAGAAATGCAAAATGAAAGCTGAGATGAGGAGGAG 180
Qy	185	CAAGAGCGAGCTGCAGGGGACTGGTGTCTGCAAACTATACATTCCTAAGCAGGCATA 244			
Db	181	CAAGAGCGAGCTGCAGGGGACTGGTGTCTGCAAACTATACATTCCTAAGCAGGCATA 240			
Qy	245	CAGATGACCTTGTGTTTTTAAACGACACACACGGTATATGAAATAATTAACAATATGA 304			
Db	241	CAGATGACCTTGTGTTTTTAACTTTTACGGTATATGAAATAATTAACAATATGA 300			
Qy	305	TTTCGTGATACAAATAGAAAACCACTGGATGAAAAATTTATTTGAGGATTTCTGGCTGA 364			
Db	301	TTTCGTGATACAAATAGAAAACCACTGGATGAAAAATTTATTTGAGGATTTCTGGCTGA 360			
Qy	365	AGAAAAGCAACGAGACTTGAGAACTTGCAAACTGAGGAAGCTGAAAGGAGGACAAAC 424			
Db	361	AGAAAAGCAACGAGAACTTGAGAACTTGCAAACTGAGGAAGCTGAAAGGAGGACAAAC 420			
Qy	425	TGATGAGCAGCGCGAATCGGAGAAAGAGGCGCGCAGATAAAGCTGACAGGGTCAAGC 484			
Db	421	TGATGAGCAGCGCGAATCGGAGAAAGAGGCGCGCAGATAAAGCTGACAGGGTCAAGC 480			
Qy	485	CAAGGTTGAGTAGAGACGAAAGAGAAATAATTTGCAATGATTTGGGTTTAGCCAGAGC 544			
Db	481	CAAGGTTGAGTAGAGACGAAAGAGAAATAATTTGCAATGATTTAGCCAGAGC 540			
Qy	545	TCCTGTTGATAATTTATGTCACATTCAGCCCATCAGACTGGCAAGAGGCTACTGTCTAG 604			
Db	541	TCCTGTTGATAATTTATGTCACATTCAGCCCATCAGACTGGCAAGAGGCTACTGTCTAG 600			

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QY 1013 TATGAGATGTTCTGTTTCTCAGAAACACATGTTTACACCGAACCACTTGAATACA 1072
Db 181 TATGAGATGTTCTGTTTCTCAGAAACACATGTTTACACTGAACCACTTGAATACA 240
QY 1073 TGTGGAACTAC-TATTGATGTCCTTAAATACCTTCTAATACAGTTTCTAATCGAAGC 1131
Db 241 TGTGMAACTACGTGGAGTGGCTTTATAATCTTATAACACAGTGTAACTGGAAGC 300
QY 1132 CAGAGTTTGTTCGATGTTCTTAAATCGTTGATGATATCCAGGTGGGTGTTGCCAC 1191
Db 301 CAGAGTTTGTTCGATGTTCTTAAACCGTGCATGCCATCCAGTGGGTGTTGCCAC 360
QY 1192 CTCAGAAGATGTCACAGCAGAAATGTTTCACACCTAAAGCAACAGTTTACGTTCCAC 1251
Db 361 CTCAGAAGATGTCACAGCAGAAATGTTTCACACTTAAAGCAACAGTTTACGTTCCGC 420
QY 1252 GAGATGCTATATGATGACATTCGTTTCTCGAGTCAGAGAGGTGGAATTTATGATA 1311
Db 421 AAGATGCTATATGATGACATTCGTTTCTCGAGTCAGAGAGGTGGAATTTATGATA 480
QY 1312 ACAGAAATCGGTTAGCATATCATATTCCTGTTTCTGAGTCAATTCGAAAGCAACACCTA 1371
Db 481 ACAGAAATCGGTTAGCATATCATATTCCTGTTTCTGAGTCAATTCGAAAGCAACACCTA 540
QY 1372 TGCACATTTGCCATATGCTGTTTGAGATGGCCCAATCG 1410
Db 541 TGCACATTTGCCATATGCTGTTTGAGATGGCCCAATCG 579

RESULT 8
CF051954/c
LOCUS OCM33a07.yg QCM Zea mays cDNA clone QCM33a07, mRNA sequence.
DEFINITION CF051954
ACCESSION CF051954
VERSION CF051954.1 GI:33091960
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 535)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
1. 535
/organism="Zea mays"
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/cultivar="F2"
/db_xref="taxon:4577"
/clone="QCM33a07"
/tissue_type="apex"
/clone_lib="QCM"

ORIGIN
Query Match 20.0%; Score 519.8; DB 14; Length 535;
Best Local Similarity 99.6%; Pred. No. 3.6e-124;
Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1494 CCAAGTACGGTTGCTTGAATCTAGCAATGTCAGAAATCTCAAAATCCATCAGATTTT 1553
Db 523 CCGAGTACGGTTGCTTGAATCTAGCAATGTCAGAAATCTCAAAATCCATCAGATTTT 464
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QY 1554 TCTTGGGTGTTTCTGAATAAATGTTGCGCTGGACTAGTCGAAGGCCCTTTGTGTTTAC 1613
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QY 1614 TTTCTGGAACCTCAAAATGGGATGTTTGGAGTCGGATATGATATATGCGAGGACGATGAC 1673
Db 403 TTTCTGGAACCTCAAAATGGGATGTTTGGAGTCGGATATGATATATGCGAGGACGATGAC 344
QY 1674 CGCCGATTTGGCTTCTCTGCTGCTCTAGAGTTTCTCCCTCCAAAGTGGATCTTCT 1733
Db 343 CGCCGATTTGGCTTCTCTGCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCT 284
QY 1734 CCGAACATAATACATATGCTATGTTGTTCAAGTCTCTCTGCTGCTGCTACACAGGAA 1793
Db 283 CCGAACATAATACATATGCTATGTTGTTCAAGTCTCTCTGCTGCTGCTACACAGGAA 224
QY 1794 AACTACGGGAAGTCTAGCTTGGCAAAACGACGGTGGTATTCACCATCCAAATCTTGAA 1853
Db 223 AACTACGGGAAGTCTAGCTTGGCAAAACGACGGTGGTATTCACCATCCAAATCTTGAA 164
QY 1854 TTTGGAGCGCATCATATTTGGCAAAAGCAATGATATTTGATATAAAGCAACACTGTCTCT 1913
Db 163 TTTGGAGCGCATCATATTTGGCAAAAGCAATGATATTTGATATAAAGCAACACTGTCTCT 104
QY 1914 AATACATATTTCAAAGGAAGTGTCAAGTCAATGTCGATGTCCTCATCTTTGGGAAATTC 1973
Db 103 AATACATATTTCAAAGGAAGTGTCAAGTCAATGTCGATGTCCTCATCTTTGGGAAATTC 44
QY 1974 TATGGCATTTCAATGGAAATGATCGGATATATGGATCCGT 2016
Db 43 TATGGCATTTCAATGGAAATGATCGGATATATGGATCCGT 1

RESULT 9
CD433067
LOCUS EL01N030401.b Endosperm_3 Zea mays cDNA, mRNA linear EST 03-JUN-2003
DEFINITION CD433067
ACCESSION CD433067
VERSION CD433067.1 GI:31348710
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 571)
AUTHORS Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
Messing,J.
TITLE Sequencing of the maize endosperm ESTs
JOURNAL Unpublished (2002)
COMMENT Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.

FEATURES
source
1. 571
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_3"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 19.8%; Score 517.4; DB 14; Length 571;
Best Local Similarity 95.3%; Pred. No. 1.6e-123;
Matches 544; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
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/mol_type="mRNA"
/cultivar="CO328"
/db_xref="taxon:4577"
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/dev_stage="4-leaf"
/clone_l1b="Zm03_RAFC_ECORC cold stressed maize seedlings"
/notes=vector: Bluescript SK+/XhoI-ECORI. Site 1: Eco RI;
Site2: Xho I; Corn seedlings at 4-leaf stage were exposed
to low temperature/high light (10C/700-8000lx/m2/s) for 4
days. plants were grown/created by J. Simmonds/l. Cass.
Library prepared by C. Piche using Stratagene kit."

```

ORIGIN

Query Match	19.9%;	Score 517.4;	DB 12;	Length 831;
Best Local Similarity	98.5%;	Pred. No. 1.8e-123;		
Matches 543;	Conservative	0;	Mismatches 6;	Indels 2; Gaps 2;
2048	TTGTGAGAAATGGTTGAAGCCACAGAGGGCTCTAAGAGGGCACTGCACGACGAAAGTTTGG	2107		
831	TTGTGTGAGAAATGGTTGAA -GCAATGAGCGTCTTAAGAGGGCACTGCACGACGAAAGTTTGG	773		
2108	GTTTACAGCAAAATCGATGTCCCGTGGTAGGAATCGTCACTCGCCTGACAGCCCAAAAGGG	2167		
772	GTTTACAGCAAAATGATGTCCCGTGGTAGGAATCGTCACTCGCCTGACAGCCCAAAAGGG	713		
2168	GATCCACCTGATCAGACATGCGATTCACGGTACACTCGAAACGGACAGGTGGTTTT	2227		
712	GATCCACCTGATCAGACATGCGATTCACGGTACACTCGAAACGGACAGGTGGTTTT	653		
2228	GCTTGGTTCAGGCGCGGACCTCTCGAATCAAAGCTGATTTTGTCAACCTGGCGAAATACGCT	2287		
652	GCTTGGTTCAGGCGCGGACCTCTCGAATCAAAGCTGATTTTGTCAACCTGGCGAAATACGCT	593		
2288	CCACGGCGTAAACCATGGGCAAGTAGGGCTTTCCTTGAACCTACGACGAGCCTCTCTCGCA	2347		
592	CCACGGCGTAAACCATGGGCAAGTAGGGCTTTCCTTGAACCTACGACGAGCCTCTCTCGCA	533		
2348	TTGTGATATAGCTGGCTCTGACTTCATCTGGTCCCATCTATATTTGAGCCTTGGCGGCT	2407		
532	TCTGATATAGCTGGCTCTGACTTCATCTGGTCCCATCTATATTTGAGCCTTGGCGGCT	474		
2408	AACCTCAGCTCGTGGCCATGGGATGGAACCATCCGATGTGCCGAAAGCTGGAGGGCT	2466		
473	AACCTCAGCTCGTGGCCATGGGATGGAACCATCCGATGTGCCGAAAGCTGGAGGGCT	414		
2468	CTTCGACACTGTCTTCGATGTGGACATGACAGGACGAGCCGAGATCGAGGCTTGA	2527		
413	CTTCGACACTGTCTTCGATGTGGACATGACAGGACGAGCCGAGATCGAGGCTTGA	354		
2528	GCCCAACGGGTTTAGCTTTTGACGAGCTGATAGCAACCGGTGTGACTACGCGCTGAAACAG	2589		
353	GCCCAACGGGTTTAGCTTTTGACGAGCTGATAGCAACCGGTGTGACTACGCGCTGAAACAG	299		
2588	GCGCATCTCAG	2598		
293	GCGCATCTCAG	283		

RESULT 11

CK247929	1014 bp	linear	EST 12-DEC-2003
LOCUS	EST731566	potato callus cDNA library, normalized and full-length	
DEFINITION	Solanum tuberosum cDNA clone POCAX21 5' end, mRNA sequence.		
ACCESSION	CK247929		
VERSION	CK247929.1	GI:39797565	
KEYWORDS	EST.		
SOURCE	Solanum tuberosum (potato)		
ORGANISM	Solanum tuberosum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Solanum tuberosum		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	asterids; lamids; Solanales; Solanaceae; Solanum.		
REFERENCE	1 (bases 1 to 1014)		

[illegible]

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RESULT 10
BG319783/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

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325 GCACCATGATGAAATTTATTTAGGATTTCTTGCTGAAGAAAGCAACGAGAACTTG 384
 578 ACCCATGATGAAATTTATTTAGGATTTCTTGCTGAAGAAAGCAACGAGAACTTG 519
 385 AGAACCTTGCAATAGGAAAGCTGAAAGGAGGAGACAACTGATGAGCGCGGAATGG 444
 518 AGAACCTTGCAATAGGAAAGCTGAAAGGAGGAGACAACTGATGAGCGCGGAATGG 459
 445 AGGAGAAAGGCGCGAGATAAGCTGACAGGGGTACAAAGCCAAAGGTTGAGGTAGACGA 504
 458 AGGAGAAAGGCGCGAGATAAGCTGACAGGGGTACAAAGCCAAAGGTTGAGGTAGACGA 399
 505 AGAAGATAAATTTGTCATATGTAATGTTAGCGAGCTCTGTTGATTAATTTATGGT 564
 398 AGAAGATAAATTTGTCATATGTAATGTTAGCGAGCTCTGTTGATTAATTTATGGT 339
 565 ACATTGAGCCCATCAGACTGGACAGAGGCTACTGTCAGATTGTTATTAACATAAACT 624
 338 ACATTGAGCCCATCAGACTGGACAGAGGCTACTGTCAGATTGTTATTAACATAAACT 279
 625 CAAGACCTCTAGTTTACAGTACTGAGATATGATGATGCTGATGCTGATTAACAAATTTGATG 684
 278 CAAGACCTCTAGTTTACAGTACTGAGATATGATGATGCTGATGCTGATTAACAAATTTGATG 219
 685 ATGACCTCTTTTCTGAAAGGCTGTTTCATCATCATGACAAAGATTGTTGATGTTGGT 744
 218 ATGACCTCTTTTCTGAAAGGCTGTTTCATCATCATGACAAAGATTGTTGATGTTGGT 159
 745 TTGAGATGTTGT 757
 158 TTGAGATGTTGT 146

RESULT 13
 CK207070
 LOCUS
 DEFINITION
 accession
 CK207070
 CK207070.1 GI:39569460
 EST
 Triticum aestivum (bread wheat)
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 1042)
 Allard, F., Crosby, M.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
 Links, M.G., McCarthy, B.L., Monroy, A., Muzak, I., Nilson, D.,
 Penniket, C., Roach, J.L. and Sarhan, F.
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops
 Unpublished (2003)
 Contact: Wm L Crosby
 Bioinformatics
 University of Saskatchewan, Department of Computer Science
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada
 Tel: 306 966 1769
 Fax: 306 966 2033
 Email: fgas.ests@cs.usask.ca
 This sequence is the direct result of the Base calling software
 Phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [16,824].
 Plate: LSB009 row: I column: 20.
 Location/Qualifiers
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 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"

/note="Vector: pCMV.SPORT6; Crown and developmental stages
 of spike formation in wheat cultivar Norstar. 4 mRNA
 populations were combined before constructing the library.
 The first mRNA population is from 1cm crown sections after
 30 days of cold acclimation. The second is from 1cm crown
 sections after 11 days of deacclimation (before
 deacclimation plants were fully vernalized for 49 days).
 The third is from different developmental stages of spike
 formation (5 to 50mm) that still have not emerged from the
 leaf (dissection required). The last is from different
 developmental stages of spike and seed formation after
 having emerged from the leaf (visible). First strand
 synthesis in this library was done in the presence of
 methylated dCTP thereby protecting from internal cleavage
 with NotI."

ORIGIN

Query Match 17.8%; Score 463.6; DB 14; Length 1042;
 Best Local Similarity 70.5%; Pred. No. 2.1e-109;
 Matches 633; Conservative 0; Mismatches 264; Indels 1; Gaps 1;

56 ATTGAAGCTGATTCACAAATTTGATCTCTATTTCAATCGTGTATCACTAGCTGTGGCAA 115
 8 AATGGTTGGAGATGGAAACCAATTTGAATCCCTTTGATACGATATCAATGTTGCTTGTCT 67
 116 TGAGCCTGATGTACTTATCAAGAGGAGCAATCAATGGGTGGAAGTGGAGATTTTCACTGA 175
 68 AAGGGGAGGATGCTTATCAAGGGGCAATCAATGGTTGGAGATGGAACCAATTTCACTGA 127
 176 AAAATTCACAGAGCGAGCTGGCGAGGAGCTGGTGTCTGCAAACTATATCACTTTCTTAA 235
 128 AAAATTCACAGAGCGAGCTGGCGAGGAGCTGGTGTCTGCAAACTATATCACTTTCTTAA 187
 236 GCAGCATACAGATGGAATTTGTTGTTTAAACGACACACGGGTATATGAAATAATAA 295
 188 GCAGCATACAGATGGAATTTGTTGTTTAAACGACACACGGGTATATGAAATAATAA 247
 296 CAATAATGATTTCTGTGATACAAATAGAAAGCAACCATGATGAAATTTATTTGAGGATTT 355
 248 TTATAATGATTTCTGTCTGATATAGAAAGTGAACGGGATGAACACTCAATTTGAGGATTT 307
 356 CTTGCTGCAAGAAAGCAACGAGACTTTGAGAACTTCGCAATAGGAGTGAAGAGAG 415
 308 CTTGCTGCAAGAAAGCAACGAGACTTTGAGAACTTCGCAATAGGAGTGAAGAGAG 367
 416 GAGACAACTGATGAGCAGCGCGCAATAGGAGAAAGAGGCGCGCAATAGGAGGCTGACAG 475
 368 AAGACAAAGCGGAGGAGGAGCGCGCAATAGGAGAAAGAGGCGCGCAATAGGAGGCTGACAG 427
 476 GGTACAAAGCAAGGTTGAGGTGAGACGAGAGAAATTAATTTGCAATGATTTGGT 535
 428 GGCACAGGCAAGGTTGAGGTGAGACGAGAGAAATTAATTTGCAATGATTTGGT 487
 536 AGCCAGAGCTCTGTTGATTAATTTGTTGATGATGAGCCCATCAGACTGGCAAGAGCG 595
 488 AGCCAGAGATATGTCGTAATTTGTTGATGATGAGCCCATCAGACTGGCAAGAGCG 547
 596 TACTGTGAGATTTGATTAATAACATTAATTTGTTGATGATGAGCCCATCAGACTGGCAAGAGCG 555
 548 TAGGGTCAGATTTGATTAATAACATTAATTTGTTGATGATGAGCCCATCAGACTGGCAAGAGCG 607
 656 GATGATGTTGGTGTATTAATAACATTAATTTGTTGATGATGAGCCCATCAGACTGGCAAGAGCG 715
 608 GTTGTGATGGGGTTTACAAATTTGTTGATGATGAGCCCATCAGACTGGCAAGAGCG 667
 716 TCAATCATGACAAAGATTTGATTTGGTGTGAGATTTGTTGATGATGAGCCCATCAGACTGGCAAGAGCG 775
 668 ATCTGAAGAAACAGGATGTTGGTGTGATGATGATGAGCCCATCAGACTGGCAAGAGCG 727
 776 TGTATTTGAGCTGGGTTTCTGTCAGCGCCCAACAGGAGGTGCAAGGAAATTTATGACAA 835
 728 GGTGTAGGACTGCGTATTAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 787

QY 836 TGGAGGACATGATTTCATCTACCTCCAAATTAACATGCTCAGGAGAGTATTGGAT 895
 Db 788 TGGGAGCAAGATTTCATCTGCGCGTTCAAAGAGCATATCCGATGACTTTGTCTTGGT 847
 QY 896 GGAAGAGAACAAAGGATCTATACAGGCTTCAACAGAGAGGAGGAAAGGAGGAG 953
 Db 848 GAAAGAGACGTAGGATAT-TTGAAGGCTTCAACGAAAGGAGGAGGAGGAGGAG 904

RESULT 14
 CD436069/c
 LOCUS EL01N0370A09.b Endospem_3 Zea mays CDNA, mRNA linear EST 03-JUN-2003
 DEFINITION CD436069
 ACCESSION CD436069.1 GI:31351712
 VERSION EST.
 KEYWORDS Zea mays
 SOURCE ORGANISM
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 791)
 Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
 Messing,J.
 Sequencing of the maize endospem ESTs
 Unpublished (2002)
 Contact: Lai, Jinsheng
 Dr. Joachim Messing's lab
 Waksman Institute, Rutgers University
 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
 Tel: 732-445-3801
 Fax: 732-445-5735
 Email: jlai@waksman.rutgers.edu
 Seq primer: T3
 Location/Qualifiers
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 /organism="Zea mays"
 /mol_type="mRNA"
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ORIGIN
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 Matches 463; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2134 TAGGAATCGTCACCTCGGCTGACAGCCCAAAAGGGATCCACCTGATCAGATCGGATTC 2193
 Db 791 TAGGAATCGTCACCTCGGCTGACAGCCCAAAAGGGATCCACCTGATCAGATCGGATTC 732
 QY 2194 ACCGTACTCGAACGGAACCGACAGGTGGTTTGGTTGGTTTCAGCGCCGACCTCGAA 2253
 Db 731 ACCGTACTCGAACGGAACCGACAGGTGGTTTGGTTGGTTTCAGCGCCGACCTCGAA 672
 QY 2254 TCCAGCTGATTTTGTCACTCGGCGATACGCTCCAGCGGCGTAACCATGGGCAAGTGA 2313
 Db 671 TCCAGCTGATTTTGTCACTCGGCGATACGCTCCAGCGGCGTAACCATGGGCAAGTGA 612
 QY 2314 GGCCTTCTTGACCTACGACGAGCTCTCTCGCATCTGATACGCTGGCTTGACTTCA 2373
 Db 611 GGCCTTCTTGACCTACGACGAGCTCTCTCGCATCTGATACGCTGGCTTGACTTCA 552
 QY 2374 TTCTGGTCCCATCTATATTTGAGCTTGGCGCTTAACCTCAGCTCTCGCATCGCGGTATG 2433
 Db 551 TTCTGGTCCCATCTATATTTGAGCTTGGCGCTTAACCTCAGCTCTCGCATCGCGGTATG 492
 QY 2434 GAAACATCCGATTTGCGCGAGACTGGAGGGCTCTTCGACACTGTCTTCGATGTGGACA 2493
 Db 491 GGACCATCCGATTTGCGCGAGACTGGAGGGCTCTTCGACACTGTCTTCGATGTGGACA 432

QY 2494 ATGACAGGAACGAGCCCGAGATCGAGCCCTTGAGCCCAACGGGTTTAGCTTTCACGAG 2553
 Db 431 ATGACAGGAACGAGCCCGAGATCGAGCCCTTGAGCCCAACGGGTTTAGCTTTCACGAG 372
 QY 2554 CTGATAGCAACGGTGTGACTACGCGCTGACAGGCGGATCTCAG 2598
 Db 371 CTGATAGCAACGGTGTGACTACGCGCTGACAGGCGGATCTCAG 327

RESULT 15
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 DEFINITION CF038283
 ACCESSION CF038283.1 GI:32933471
 VERSION EST.
 KEYWORDS Zea mays
 SOURCE ORGANISM
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 466)
 Genoplatne, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplatne
 Genoplatne
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>
 and <http://genoplatne-info.infobiogen.fr>).

FEATURES
 Location/Qualifiers
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 2.5e-108;
 Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1558 GGGGTGGTTCTGAAATAAATGTGTGGCGTGAGTGTGCGAGGCGCTTTGTGTTTACTTCC 1617
 Db 459 GGGGTGGTTCTGAAATAAATGTGTGGCGTGAGTGTGCGAGGCGCTTTGTGTTTACTTCC 400
 QY 1618 TGGAACTTCAAAATGGATGTTTGGAGTCGGATATGATGCGAGGAGATGACCGCC 1677
 Db 399 TGGAACTTCAAAATGGATGTTTGGAGTCGGATATGATGCGAGGAGATGACCGCC 340
 QY 1678 GATTGTGCTTCTTCTGCTGCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCGGA 1737
 Db 339 GATTGTGCTTCTTCTGCTGCTGCTCTAGAGTTTCTCTCCAAAGTGGATCTTCTCGGA 280
 QY 1738 ACATAATACATGTCATGATGTTGGTCAAGTGTCTGTTGGCTGGCTACACAGGAAACT 1797
 Db 279 ACATAATACATGTCATGATGTTGGTCAAGTGTCTGTTGGCTGGCTACACAGGAAACT 220
 QY 1798 ACGGAAGTCTAGCTTGGCAAAACCGACGGGTGATTCACCATCCAAATCTTGAATTG 1857
 Db 219 ACGGAAGTCTAGCTTGGCAAAACCGACGGGTGATTCACCATCCAAATCTTGAATTG 160
 QY 1858 GAGCGCATCATTTGGCAAAACCAATGAGATATTGTGATAAAGCAACACTGTCTCTAATA 1917
 Db 159 GAGCGCATCATTTGGCAAAACCAATGAGATATTGTGATAAAGCAACACTGTCTCTAATA 100

